FIGURE 1

PANEL A

proteIn
subunits

avidin

template

5'

3'

elution with
displacement oligonucleotide

PANEL B

avidin

template

5'

3'

FIGURE 2

FIGURE 3

NXT   Heparin   Affinity   Glyc.grad.

1 2 3 4 5 6 7 8 9 10 11 12 13

100%   62%   132%   50%

relative activity/pmol telomerase

FIGURE 4

Glyc. grad. fractions

pmol BSA

M   0.5   1.5   4.5   15

170 —
116 —
43 —
14 —

1   2   3   4   5   6   7   8   9

1 pmol telomerase RNP

FIGURE 5

FIGURE 6

FIGURE 7

telomerase

3'   5'

                    template

CCAAAACCCCAAAAC

           TTTTGGGG-3'

PANEL A

telomerase

3'   5'

                    template

CCAAAACCCCAAAAC

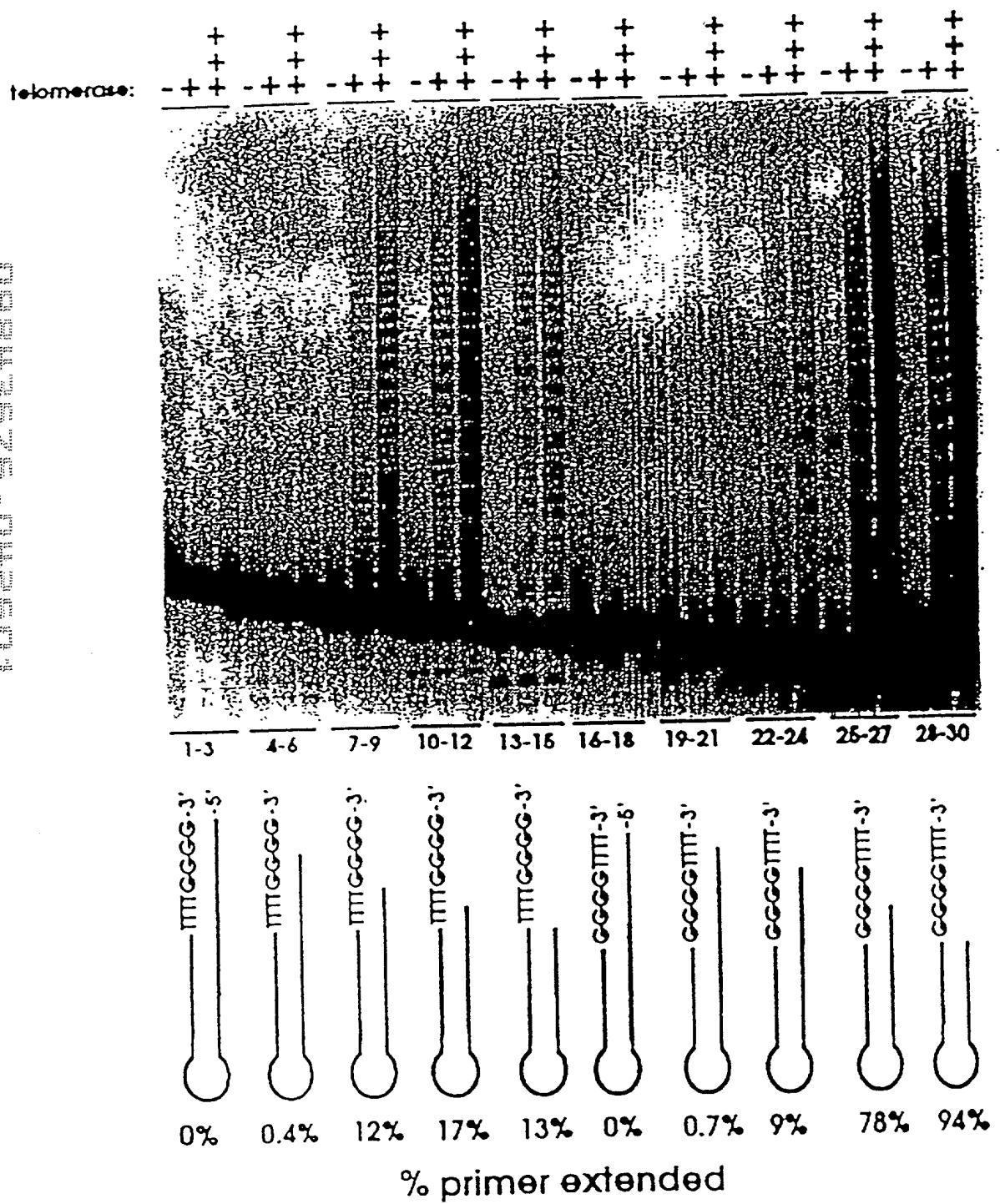   CCGTTTT-3'
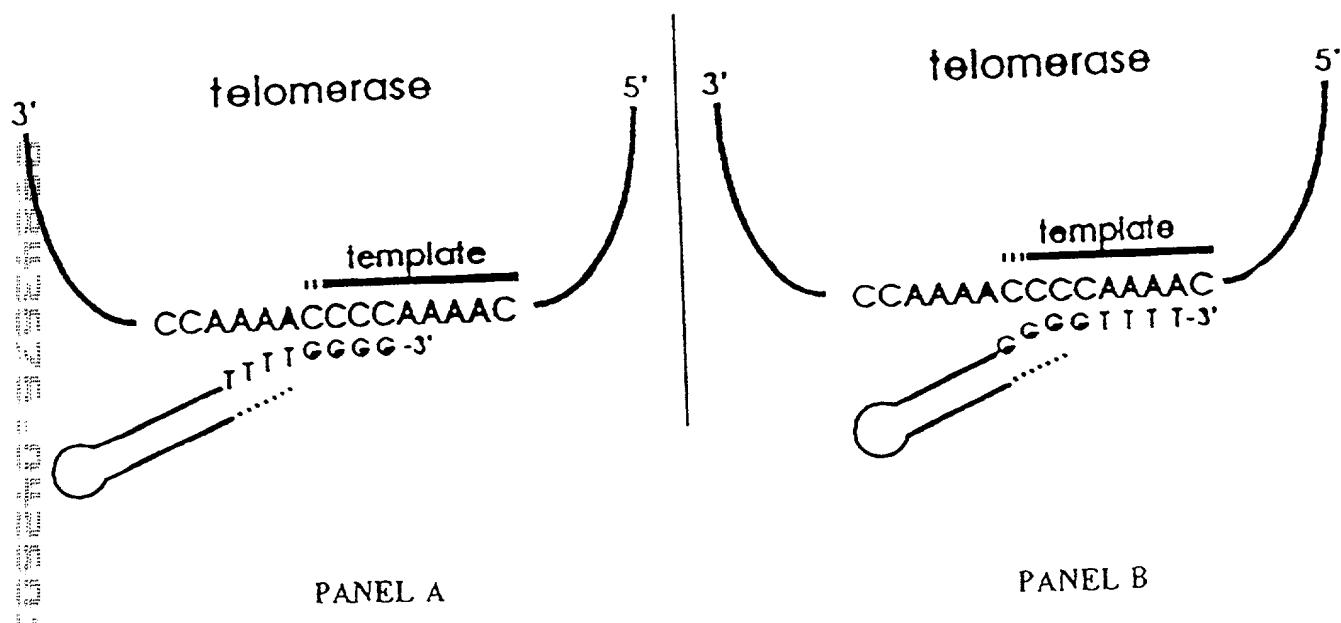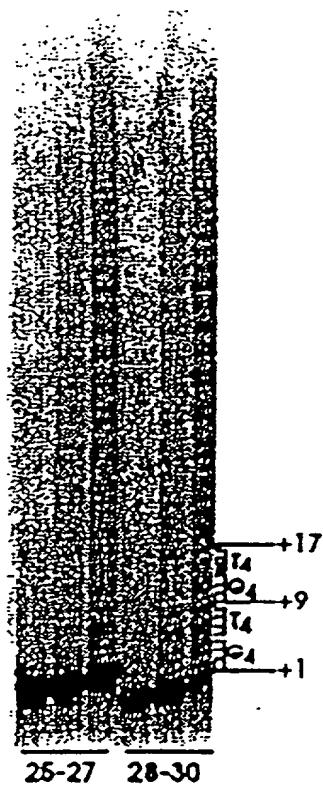
PANEL B

FIGURE 8

26-27   28-30

FIGURE 9

```
   1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
  51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
 101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
 151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
 251 TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG
 301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT
 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTCA
 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
 501 CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
 551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
 601 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
 651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA
 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
 801 ATATGAAATC AAGAACCAGA ATATTTATT GCACTCATTT TAATAGAAAT
 851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC
 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
 951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG
1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACTTGA
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
1151 TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA
1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
1251 AAAAGAAAGT TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC
1301 AAAAACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
1351 GGTTGAGACC TCTGCAAAGC ATTTTTATTA TTTTGATCAC GAAAACATCT
1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
1451 CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
1701 TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC GAAGTTATTG
1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
1801 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
1851 AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAACTATC
1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA
2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
2101 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG
2151 AACAAAATGA CTTAAATGCA AAGAAACAT TAATTGTTGA AGCAAAGCAA
2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG
2251 CCAATATAAT TACATTAACT TTAATGGGAA GTTTTATAAA CAAACAAAAG
2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTCATC ATTTTATTAT
```

FIGURE 9 (cont.)

```
2351  GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
2401  CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451  TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
2501  ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA
2551  GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601  GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651  TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701  AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751  CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
2801  CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACTCT
2851  CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901  AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC
2951  TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001  CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051  ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101  AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
3151  GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201  CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTTG TCTTATATAC
3251  TGGGGTTTTG GGGTTTTGGG GTTTTGGGG
```

FIGURE 10

```
   1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
  51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
 101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
 151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA
 201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNNMKSRTR IFYCTHFNRN
 251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAYM
 301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
 351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELIH
 401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWIFEDLVVS
 451 LIRCFFYVTE QQKSYSKTYY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
 501 EEWKKSLGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL
 551 NSHLMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
 601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
 651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLIVEAKQ
 701 RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY
 751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIEKL
 801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
 851 SIDMKTLALM PNINLRIEGI LCTLNLMQT KKASMWLKKK LKSFLMNNIT
 901 HYFRKTITTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID
 951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
1001 KYIFNRVCMI LKAKEAKLKS DQCQSLIQYD A
```

FIGURE 11

```
   1 CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAAGA AAAAATTGAG
  51 GTAGTTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA
 101 TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
 151 GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
 201 TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
 251 CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA
 301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
 351 AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA
 401 TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTC
 451 CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
 501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
 551 AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCG
 601 TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
 651 TTGAGACAAT TGAAAAAGCT GTTTACAACT GAAGGAATCG CAGTTCTGAA
 701 AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
 751 CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT
 801 TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
 851 TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC
 901 TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
 951 AAAAGAAGCA GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT
1001 TTGTTGATTC TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA
1051 AAAGAAGAAG AGCTATCACA ATCCTGATTC TTAAAGATTT CAAAAATTCC
1101 AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG TTTTTCATTT
1151 CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA
1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT
1251 TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA
1301 GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
1351 AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA
1401 AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG
1451 ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATTA AAGAAATAAA
1501 GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA
1601 ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAGAAGA CCAGTTAGCA
1651 AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
1701 AAGATTTATT TTTTTCAATA ATTTATTGAA AAGAGGGGGTT TTGGGGTTTT
1751 GGGGTTTTGG GG
```

FIGURE 12

```
    CCCCAAAACCCCAAAACCCCAAAACCCCTATAAAAAAAGAAAAAATTGAGGTAGTTTAGA
  1 --------+---------+---------+---------+---------+---------+  60
    GGGGTTTTGGGGTTTTGGGGTTTTGGGGATATTTTTTTCTTTTTTAACTCCATCAAATCT

a    P  Q  N  P  K  T  P  K  P  L  *  K  K  K  K  L  R  *  F  R   -
b    P  K  T  P  K  P  Q  N  P  Y  K  K  R  K  N  C  G  S  L  E   -
c    P  K  P  Q  N  P  K  T  P  I  K  K  E  K  I  E  V  V  *  K   -

    AATAAAATATTATTCCCGCACAAATGGAGATGGATATTGATTTGGATGATATAGAAAATT
 61 --------+---------+---------+---------+---------+---------+ 120
    TTATTTTATAATAAGGGCGTGTTTACCTCTACCTATAACTAAACCTACTATATCTTTTAA

a    N  K  I  L  F  P  H  K  W  R  W  I  L  I  W  M  I  *  K  I   -
b    I  K  Y  Y  S  R  T  N  G  D  G  Y  C  F  G  C  *  Y  R  K  F  -
c    *  N  I  I  P  A  Q  M  E  M  D  I  D  L  D  D  I  E  N  L   -

    TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA
121 --------+---------+---------+---------+---------+---------+ 180
    ATGAAGGATTATGTAAGTTGTTCATATCGTCGAGAACATCACTGTTCTTTCCTACGTTTT

a    Y  F  L  I  H  S  T  S  I  A  A  L  V  V  T  R  K  D  A  K   -
b    T  S  *  Y  I  Q  Q  V  *  Q  L  L  *  *  Q  E  R  M  Q  N   -
c    L  P  N  T  F  N  K  Y  S  S  S  C  S  D  K  K  G  C  K  T   -

    CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
181 --------+---------+---------+---------+---------+---------+ 240
    GTAACTTTAGACCGAGCTTTAGCGGAAGTAACTGATAAGGTTTCAACGTTTTTGTTAATC

a    H  C  N  L  A  R  N  R  L  H  C  L  F  Q  S  C  K  N  N  *   -
b    I  E  I  W  L  E  I  A  F  I  D  Y  S  K  V  A  K  T  I  R   -
c    L  K  S  G  S  K  S  P  S  L  T  I  P  K  L  Q  K  Q  L  E   -

    AGTTCTACTTCTCGGATGCAAATCTTTATAACGATTCTTTCTTGAGAAAATTAGTTTTAA
241 --------+---------+---------+---------+---------+---------+ 300
    TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTTAATCAAAATT

a    S  S  T  S  R  M  Q  I  F  I  T  I  L  S  C  E  N  *  F  *   -
b    V  L  L  L  G  C  K  S  L  *  R  F  F  L  E  K  I  S  F  K   -
c    F  Y  F  S  D  A  N  L  Y  N  D  S  F  L  R  K  L  V  L  K   -

    AAAGCGGAGAGCAAAGAGTAGAAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA
301 --------+---------+---------+---------+---------+---------+ 360
    TTTCGCCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTAGTCCATT

a    K  A  E  S  K  E  *  K  L  K  H  Y  *  C  L  N  K  I  R  *   -
b    K  R  R  A  K  S  R  N  C  N  I  T  N  V  *  I  K  S  G  N   -
c    S  G  E  Q  R  V  E  I  E  T  L  L  M  F  K  *  N  Q  V  M   -

    TGACGATTATTCTATTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA
361 --------+---------+---------+---------+---------+---------+ 420
    ACTGCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT

a    C  G  L  F  Y  F  L  D  H  F  L  R  S  I  M  E  K  I  T  *   -
b    E  D  Y  S  I  F  *  I  T  S  *  G  A  L  W  R  K  L  L  N   -
c    R  I  I  L  F  F  R  S  L  L  K  E  H  Y  G  E  N  Y  L  I   -

    TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT
421 --------+---------+---------+---------+---------+---------+ 480
    ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTTAA

a    Y  *  K  V  N  S  L  D  Y  F  P  S  Q  Q  C  C  V  Y  *  I   -
b    T  K  R  *  T  V  W  I  I  S  L  A  N  N  D  E  Y  I  K  F   -
c    L  K  G  K  Q  F  G  L  F  P  *  P  T  M  M  S  I  L  N  S   -
```

FIGURE 12 (cont.)

```
         CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT
   481   ------------------------------------------------------------   540
         GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA

    a      H  M  R  M  S  Q  R  I  S  I  H  Q  T  Y  Q  R  Q  T  R  Y  -
    b      I  C  E  C  V  K  G  S  R  Y  I  R  L  T  K  D  K  L  A  I  -
    c      Y  E  N  E  S  K  D  L  D  T  S  D  L  P  K  T  N  S  L  *  -


         AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTCG
   541   ------------------------------------------------------------   600
         TTTTGCGTTCTTTTTCAAACTATTAGCTTGTCGTCTTCTTGAATAACGTAAATGATAAGC

    a      K  T  Q  E  K  V  C  *  S  N  S  R  R  T  Y  C  I  Y  Y  S  -
    b      K  R  K  K  K  F  D  N  R  T  A  E  E  L  I  A  F  T  I  R  -
    c      N  A  R  K  S  L  I  I  E  Q  Q  K  N  L  L  H  L  L  F  V  -


         TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACTCCCGAGTCTTGAGACAAT
   601   ------------------------------------------------------------   660
         ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA

    a      Y  G  F  Y  Y  N  C  F  R  Y  R  R  C  T  P  E  S  C  D  N  -
    b      M  G  F  I  T  I  V  L  G  I  D  G  E  L  P  S  L  E  T  I  -
    c      W  V  L  L  Q  L  F  *  V  S  T  V  N  S  R  V  L  R  Q  L  -


         TGAAAAAGCTGTTTACAACTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT
   661   ------------------------------------------------------------   720
         ACTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA

    a      C  K  S  C  L  Q  L  K  E  S  Q  F  C  K  F  *  C  V  C  H  -
    b      E  K  A  V  Y  N  C  R  N  R  S  S  E  S  S  D  V  Y  A  I  -
    c      K  K  L  F  T  T  E  G  I  A  V  L  K  V  L  M  C  M  P  L  -


         TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA
   721   ------------------------------------------------------------   780
         ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT

    a      Y  F  V  N  *  S  Q  I  S  Y  L  N  L  M  D  S  Y  R  N  K  -
    b      I  L  C  I  N  L  K  Y  L  I  S  I  *  W  I  A  I  E  T  N  -
    c      F  C  E  L  I  S  N  I  L  S  Q  F  N  G  *  L  *  K  Q  T  -


         CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC
   781   ------------------------------------------------------------   840
         GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG

    a      P  N  K  P  C  K  F  N  G  I  Y  V  K  S  F  G  T  N  A  H  -
    b      Q  I  N  H  A  S  L  M  E  Y  T  L  N  P  L  G  Q  M  H  T  -
    c      K  *  T  M  Q  V  *  W  N  I  R  *  I  L  W  D  K  C  T  L  -


         TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC
   841   ------------------------------------------------------------   900
         ACTTAAATATAACCTAAGAATTTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG

    a      C  I  Y  I  G  F  L  K  H  R  Y  T  E  C  F  R  D  C  F  S  -
    b      E  F  I  L  D  S  *  S  I  D  T  Q  N  A  L  E  T  D  L  A  -
    c      N  L  Y  W  I  L  K  A  *  I  H  R  M  L  *  R  L  I  *  L  -


         TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA
   901   ------------------------------------------------------------   960
         AATGTTGTCTAATGGACAAAACTAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT

    a      L  Q  Q  I  T  C  F  D  Y  S  C  S  S  L  I  S  L  K  E  A  -
    b      Y  N  R  L  P  V  L  I  T  L  A  H  L  L  Y  L  *  K  K  Q  -
    c      T  T  D  Y  L  F  C  L  L  L  L  I  S  Y  I  F  K  R  S  R  -


         GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC
   961   ------------------------------------------------------------   1020
         CCGCTTTACTTTTCTTCTGATTTCTTTCTCTAAAGTTTTAAACAACTAAGAAGACATTGG

    a      G  E  M  K  R  R  L  K  K  E  I  S  K  F  V  D  S  S  V  T  -
    b      A  K  *  K  E  D  *  R  K  R  F  Q  N  L  L  I  L  L  *  P  -
    c      R  N  E  K  K  T  K  E  R  D  F  K  I  C  C  F  F  C  N  R  -


         GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAAGAGCTATCACAATCCTGATTC
   1021  ------------------------------------------------------------   1080
         CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTTCTCGATAGTGTTAGGACTAAG

    a      G  I  N  N  K  N  I  S  N  E  K  E  E  E  L  S  Q  S  C  F  -
    b      E  L  T  T  R  I  L  A  T  K  K  K  K  S  Y  H  N  P  D  S  -
    c      N  *  Q  Q  E  Y  *  Q  P  K  R  R  R  A  I  T  I  L  I  L  -
```

FIGURE 12 (cont.)

```
        TTAAAGATTTCAAAAATTCCAGGTAAGAGAGATACATTCATTAAAAATTCATATATTATAG
1081    ------------+---------+---------+---------+---------+---------+    1140
        AATTTCTAAAGTTTTTAAGGTCCATTCTCTCTATGTAAGTAATTTTAAGTATATAATATC

a         L  K  I  S  K  I  P  G  K  R  D  T  F  I  K  I  H  I  L  ·   -
b         ·  R  F  Q  K  F  Q  V  R  E  I  H  S  L  K  F  I  Y  Y  S   -
c         K  D  F  K  N  S  R  ·  E  R  Y  I  H  ·  N  S  Y  I  I  V   -

        TTTTTCATTTCACAGCTGTTATTTTCTTTTATCTTAACAATATTTTTTGATTAGCTGGAA
1141    ------------+---------+---------+---------+---------+---------+    1200
        AAAAAGTAAAGTGTCGACAATAAAAGAAAATAGAATTGTTATAAAAAACTAATCGACCTT

a         F  F  I  S  Q  L  L  F  S  F  I  L  T  I  F  F  D  ·  L  E   -
b         F  S  F  H  S  C  Y  F  L  L  S  ·  Q  Y  F  L  I  S  W  K   -
c         F  H  F  T  A  V  I  F  F  Y  L  N  N  I  F  C  L  A  G  S   -

        GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAACTTAGCTTATTCACATTCAT
1201    ------------+---------+---------+---------+---------+---------+    1260
        CATTTTTCATAGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAGTA

a         V  K  S  I  K  ·  E  K  R  ·  T  E  V  T  ·  L  I  H  H   -
b         ·  K  V  S  N  K  R  S  A  R  L  R  ·  L  S  L  F  T  F  I   -
c         K  K  Y  Q  I  R  E  A  L  D  C  G  N  L  A  Y  S  H  S  ·   -

        AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA
1261    ------------+---------+---------+---------+---------+---------+    1320
        TCTAGCTGGAAGTATATAGGTTATGCTACTATTCCTTTGTCGTCAGTAGGCAAAATTTTT

a         R  S  T  F  I  Y  P  I  R  C  ·  G  N  S  S  H  P  F  ·  K   -
b         D  R  P  S  Y  I  Q  Y  D  D  K  E  T  A  V  I  R  F  K  N   -
c         I  D  L  H  I  S  N  T  M  I  R  K  Q  Q  S  S  V  L  K  I   -

        TAGTGCTATGAGGACTAAATTTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA
1321    ------------+---------+---------+---------+---------+---------+    1380
        ATCACGATACTCCTGATTTAAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT

a         ·  C  Y  E  D  ·  I  F  R  V  K  K  W  S  R  N  L  N  Q  K   -
b         S  A  M  R  T  K  F  L  E  S  R  N  G  A  E  I  L  I  K  K   -
c         V  L  C  G  L  N  F  ·  S  Q  E  M  E  P  K  S  ·  S  K  R   -

        GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTCGTTAATAAGTATTACCA
1381    ------------+---------+---------+---------+---------+---------+    1440
        CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTTAGAAAGCAATTATTCATAATGGT

a         E  L  R  R  Y  C  K  R  I  E  L  ·  I  F  R  ·  ·  V  L  P   -
b         N  C  V  D  I  A  K  E  S  N  S  K  S  F  V  N  K  Y  Y  Q   -
c         I  A  S  I  L  Q  K  N  R  T  L  N  L  S  L  I  S  I  T  N   -

        ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA
1441    --------------+---------+---------+---------+---------+--------    1500
        TAGAACTAACTAACTTCTCTAACTGCTCCGTTGACGTGTCTTCTAGTAATTTCTTTATTT

a         I  L  I  D  C  R  D  ·  R  G  N  C  T  E  D  H  ·  R  N  K   -
b         S  C  L  I  E  E  I  D  E  A  T  A  Q  K  I  I  K  E  I  K   -
c         L  D  C  L  K  R  L  T  R  Q  L  H  R  R  S  L  K  K  ·  S   -

        GTAACTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA
1501    ------------+---------+---------+---------+---------+---------+    1560
        CATTGAAAATAATTAATCTCTTATTTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT

a         V  T  F  I  N  ·  R  I  N  ·  I  T  N  I  E  I  S  D  L  Q   -
b         ·  L  L  L  I  R  E  ·  T  K  L  L  I  ·  R  S  A  I  F  N   -
c         N  F  Y  ·  L  E  N  K  L  N  Y  ·  Y  R  D  Q  R  S  S  I   -

        TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAAATACAAACCTTGGTCAAAAT
1561    ------------+---------+---------+---------+---------+---------+    1620
        AACTGCTTTATTTTCGACTTGATTTCAATCTGTTATTTTTTATGTTTGGAACCAGTTTTA

a         L  T  K  ·  K  L  N  ·  S  ·  T  I  K  N  T  N  L  G  Q  N   -
b         C  R  N  K  S  C  T  K  V  R  Q  ·  K  I  Q  T  L  V  K  I   -
c         D  E  I  K  A  E  L  K  L  D  N  K  K  Y  K  P  W  S  K  Y   -

        ATTGAGGAAGGAAAAGAAGACCAGTTAGCAAAAGAAAAAATAAGGCAATAAATAAAATGA
1621    ------------+---------+---------+---------+---------+---------+    1680
        TAACTCCTTCCTTTTCTTCTGGTCAATCGTTTTCTTTTTTATTCCGTTATTTATTTTACT

a         I  E  E  G  K  E  D  Q  L  A  K  E  K  I  R  Q  ·  I  K  C   -
b         L  R  K  E  K  K  T  S  ·  Q  K  K  K  ·  G  N  K  ·  N  E   -
c         C  G  R  K  R  R  P  V  S  K  R  K  N  K  A  I  N  K  M  S   -
```

FIGURE 12 (cont.)

```
      GTACAGAAGTGAAGAAATAAAAGATTTATTTTTTTCAATAATTTATTGAAAAGAGGGGTT
1681  ------------------+-----------+------------+------------+---------+  1740
      CATGTCTTCACTTCTTTATTTTCTAAATAAAAAAAGTTATTAAATAACTTTTCTCCCCAA
```

```
a     V  Q  K  C  R  N  K  R  F  I  F  F  N  N  L  L  K  R  G  V  -
b     Y  R  S  E  E  I  K  D  L  F  F  S  I  I  Y  C  K  E  G  F  -
c     T  E  V  K  K  *  K  I  Y  F  F  Q  *  F  I  E  K  R  G  F  -
```

```
      TTGGGGTTTTGGGGTTTTGGGG
1741  ----------------+--------+--- 1762
      AACCCCAAAACCCCAAAACCCC
```

```
a     L  G  F  W  G  F  G     -
b        W  G  F  G  V  L  G  -
c           G  V  L  G  F  W  -
```

FIGURE 13

```
  2 EVDVDNQADNHGIHSALKTCEEIKEAKTLYSWIQKVIRCRNQSQSHYKDL  51
    |.    |   ..|.  :|    |.::|  .    :.  |  |..|.|.|
 19 ELELEMQENQNDIQVRVK.  .IDDPKQY..LVNVTAACLLQEGSYYQDK  62

 52 EDIKIFAQTNIVATPRDYNEEDFKVIARKEVF.STGLMIELIDKCLVELL 100
    .                ..| .|.. |:  ..:| |   ....:.|..
 63 DERRYIITKALL     .EVAESDPEFICQLAVYIRNELYIRTTTNYIVAF. 107

101 SSSDVSDRQKLQCFGFQLKGNQLAKTHLLTALSTQKQYFFQDEWNQVRAM 150
                              .|.  ...:.  |  ||   :
108          CVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYI 144

151 IGNELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDHLKVNDKFDKKQKGGA 200
    ..  :  ||        |.  .:  :.:: ..|.... ::    ::
145 FDATEFKNLY      ....  ..LDRILSQDIRKELTFRKCLQRCVRSKF 181

201 ADMNE   PRCCSTCKYNVKNEKDHFLNNINVPNWNNMKSRTRIFYCTHF 247
    .|:      |    .|...|. |..|. |  |..|.. |.:
182 SEFNEYQLGKYCTES. QRKKTMFRYLSVTNKQKWDQTKKK.       . 220

248 NRNNQFFKKHEFVSNKNNISAMDRAQTIFTNIFRFNRIRKKLKDKVIEKI 297
    |  |  |: .  .:|    :    :|:..: | ||. |:.||
221 .RKENLLTKLQAIKESEDKSKRETG...  .DIMNVEDAIKALKPAVMKKI 264

298 AYMLEKVKDFNFNYYLTKSCPLPENWRERKQKIENLINKTREEKSKYYEE 347
    |    |            .. | ..: |.| |.|    :.:
265 AKRQNAMK..        ....  .....KHMKAPKIPNSTLESKYLTFKD 294

348 LFSYTTDNKCVTQFINEFFYNILPKDFLTGRNRKNFQKKVKKYVELNKHE 397
    |:.  .   .|  .|.||.|.: .. .   ..:| .|
295 LIKFCHISEP   ..KERVYKILGKKYPKTEEEYKAAFGDSASAPFN.PE 338

398 LIHKNLLLEKINTREISWMQVETSAKHFYYFDHENIYVLWKLLRWIFEDL 447
    | |  .| .|:|  .: ...|.  .| ...  :||  :
339 LAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSN.. 386

448 VVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQE 497
                        |:|  ::.|
387                  ..  .....ILKAGVSD...   .. 394

498 KEVEEWKKSLGFAPGKLRLIPKKTTFRPIMTFNKKIVNSDRKTTKLTTNT 547
                                          ||:.
395              .   .  ...  .........  .TTHS 398

548 KLLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL 597
    |                             :|. |.|:..|·
399 IVINK            .  .....  ....ICEPKAVENSKM 415

598 FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNNIVID 647
    |   :      || | .  .:|..|   .:   ::|| |:  |::
416 F  PLQFFSAIEAVN.EAVTKGFKAKK...RENMNLKGQIEAVKE..VVE 457

648 SKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKTLIVE 697
    .. |:|          -||..: ..:.| |. ...  ..| :.
458 KTDEEKKDM      .....ELEQTEEGEFVKVNEGIGKQYINSIELAIK 496

698 AKQRNYFKKDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSS 747
    .  :..    :::.  . .    |  ::. .| ..: :|:
497 IAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGL 546

748 FYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFI 797
    :  .|.||: ·:...| ..:. ::: :
547 MVKQRCEKSSFYIFSSPSSQCNKCYLEVDL................... 576

798 EKLINVSRENGFKFNMKK.LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846
    ·:·. .|.| ||.. .|:.. ...: ::::| ...|
577  ..   PGDELRPSMQKLLQEKGKLGGG..TDFPYECIDEWTKNKTHVD 617

847 WIGISIDMKTLALMPNINLRIEGILCTLNLNMQTKKASMWLKKKLKSFLM 896
    |.| ||..  .:||:| .:|:  :                ||.|. :
618 NIVILSDMMIAEGYSDINVRGSSIVNSI............ ..KKYKDEVN 653

897 NNITHYFRKTITTEDFANKTLNKLFISGGYKYMQCAKEYKD.HFKKNLAM 945
    ||.:  .:. |:.:              |:: :.|:.: :| | :|
654 PNIKIF. .AVDLEGYG............ ...KCLNLGDEFNENNYIKIFGM 687

946 SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIE 995
    |.|               :|:: .. .. ...|
688 SDSI........   .....LKFISAKQGGA........ ... .NMVE 706

996 IFSTKKYIFNRVC 1008
    ::  |.: :.::.
707 VI..KNFALQKIG 717
```

FIGURE 14

```
132 LSTQKQYFFQDEWNQVRAMIGNEL.FRHLYTKYLIFQRTSE..GTLVQFC 178
    :| ..|        ...| |||| .  :. .. ::..   |  | |
  1 MSRRNQ.   ...KKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQI 43

179 GNNVFDHLKVNDKFDKKQKGGAADMNEPRCCSTCKYNVKNEKDHFLNNIN 228
    :  .. ||   . . ..|.. | |        | .|...:.:|.. |
 44 KEEDLKLLKFKNQDQDGNSGNDDDDEE..   ...NNSNKQQELLRRVN 84

229 VPNWNNMKSRTRIFYCTHFNRNNQFFKKHEFVSNKNNISAMDRAQTIFTN 278
               .. . |:|| |:.| : .   ...: .|
 85  ..          .QIKQQVQLIKK. .VGSKVEKDLNLNEDENKKN 114

279 IFRFNRIRKKLKDKVIEKIAYMLEKVKDFNFNYYLTKSCPLPENWRERKQ 328
    :. . .      .|     . | ::::.. |..|... . ::|| .
115 GLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRETDY 164

329 KIENLINKTREEKSKYYEELFSYTTDNKCVTQFINE.FFYNILPKDFLTG 377
    ..|.::. ..:.|          .:|. : |:   |  : ||::.
165 DTEKWFEISHDQK .   ..... . NYVSIYANQKTSYCWWLKDYFNK 200

378 RNRKNFQKKVKKYVELNKHELIHKNLLLEKINTREISWMQVETSAKHFYY 427
    .| ::. ...      .|.. : : :.| . :|: |:..
201 NNYDHLNVSINRLE. TEAEFYAFDDFSQTIKLTNNSYQTVNID..... 242

428 FDHENIYVLWKLLRWI..FEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNI 475
    : :| .    ||| . |. - ||: : | .| .:.|.    ..|
243 VNFDNNLCILALLRFLLSLERFNILNIRSSY..TRNQYNFEKIGELLETI 290

476 WDVIMKHSIADLKKETLAEVQEKEVEEWKKSLGFAPGKLRLIPKKTTFRP 525
    :.|:. .          |:  .. ..:. .. |. |.
291 FAVVFSHR       HLQGIHLQVPCEAFQYLVNSSSQISVXDSQLQ 330

526 IMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDPFGFAVFNY 575
    : .| ..  |  |.| . |:|.. |. |   . |  . || |.
331 VYSFSTDLKLVD. TNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENL 378

576 DDVMKKYEEFVCKWKQVGQPKLF.    ..FATMDIEKCYDS..VNREK 615
    : :|| .         :. .||. . : .. :: |
379 NVLLKKVKH  ANLNLVSIPTQFNFDFYFVNLQHLKLEFGLEPNILTKQK 426

516 LSTFL    KTTKLLSSDFWIMTAQILKRKNNI  VIDSKNFRKKEMK 657
    |. |     |  | | | | || ||.  ... ||::.
427 LENLLLSIKQSKNLKFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQ 476

558 DYFRQKFQKIALEGGQYPTLFSVLEN  EQNDLNAKKTLIVEAKQRNYFK 705
    |  |     : | | |: : .:|.| |
477 EETPETKDETPSESTSGMKFFDHLSELTELEDFSVN . LQATQEIY 520

706 KDNELQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYYATLEE 755
    | |    .  |       | .. |      | ||
521 .DSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNI.  . YETLNN 564

756 SSLGFLRDESMNPENPNVNLLHRLTDDYLLITTQENNAVLFIEKLINVSR 905
        | ; || ; || ....: ||
565     LKRCSVNISNPHGNISYELTN . ..KDSTFYKFKLTLNQE 600

806 ENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMK 855
        |  | | | | || .|:|. : ::..|..|: : .:.
601 LQHAKYTFK  QNEFQFNNVKSAKIESSSLESLEDIDSLCKSIASCKNLQ 648

856 TLALMPNINLRIEGILCTLNLNMQT KKASMWLKK..KLKSFLMNNITH 901
    .:..       |  .| |  . |.. :::|. .||.:   .|.
649 NVNI.      IASLLYPNNIQKNPFNKPNLLFFKQFEQLKNLENVSINC 691

902 YFRKTI   TTEDFANKTLNKLFISGGYKYMQCAKEYKDHFKKNLAMSSM 948
    |    |    . |  | || | .:|: :|.. ||.  .:...
692 ILDQHILNSISEFLEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPEL 741

949 IDLEVSKIIYSVT        RAFFKYLVCNIKDT. IFGEEHY 982
    ..        |          :||:. | ||:. .. .:
742 NQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDF 791

983 PDFFLS TLKHFIEIFSTKKY IFNRVCMILKAKEAKLKSDQCQSLIQ 1028
    |  | | | | il |   ... | ...::.|.|:
792 DQNTVSDDSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLK 840
```

FIGURE 15

```
  4 DIDLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPSLTIPK...... 47
    ..||.         ....| |.. :||.|.... :|| .|.
617 NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNP 666

 48         LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVE....IETLLM 86
           || |       |:  ::| -| | .: :|   |..::.
667 FNKPNLLFFKQFEQLKNLENVSINCILDQHILNSISEFLEKNKKIKAFIL 716
```

FIGURE 16

```
  1  MEMDIDLDDIENL    . LPNTFNKYSSSCSDKKGCKTLKSGSKSPS.    42
     :  :        ::        ..:.. :-: :....:. . : :: ..:
491  IELAIKIAVNKNLDEIKGHTAIFSDVSGSHSTSMSGGAKKYGSVRTCLEC  540

 43  LTIPKLQKQ     .LEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLL  85
     :        ::     : .. :... ::.-:: .. :.::: :..-::-::
541  ALVLGLMVKQRCEKSSFYIFSSPSSQCNKCYL.EVDLPGDELRPSMQKLL  589
```

FIGURE 17

Motif A   Motif B

```
                        h--h-Dh---h--h                              h---+-DG---SP
Consensus
telomerase p123    GQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLL-100-KFYKQTKGIPQELCVSSILSSFYYATLEESSLGFL
Dong (LINE)        KNRNLHCTYIDYKKAFDSIPHSVLIQVLEIYKIN- 28-RQLAIKKGIYQDSLSPWFCLALNPLSHQLHNDR
al S.c.(groupII)   FGGSNWFREVDLKKCFDTISHDLIIKELKRYISD- 26-HVPVGPRVCVQCAPTSPALCNAVLRLDRRLAGLA
HIV-RT             LKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP-  7-GIRYQYNVLPQGWKGSPAIFQSSMTKILEPFRKQN
L8543.12 yeast     VLPELYFMKFDVKSCYDSIPRMECMRILKDALKN- 68-KCYIREDGLFQESSLSA?IVDLVYDDLLEFYSEPK
```

Motif C   Motif D   Motif B

```
                        h--YhDDhhh               Gh-h---K            h-hiGh-h
Consensus
telomerase p123    -14-LMRLTDDYLLITTQENN-0-AVLFIEKLINVSRENCFKPNMRKLQT-23-QDYCDWIGISI
Dong (LINE)        -16-HLIYMDDIKLYAKNDKE-0-MKKLIDTTIFSNDISMQPGLLDKCKT-25-KCJYKYLGFQQ
al S.c.(groupII)   -55-YVRYADDILIGVLGSKN-2-KIIKRDLNNFLNS.IGLTINEEKTLI: 4-ETPARFLGYNI
HIV-RT             - 4-IYQYMDDLYVGSHLEIG-1-HRTKIEELRQHLLRWGLTTPDRKHQK- 0-EPPFLWMGYEL
L8543.12 yeast     - 8-ILKLADDFLIISTDQQQ......VINIKKLAMGFQKYNAHANR-41-IRSKSSKGIFR
```

FIGURE 18

```
telomerase p43   LQKQIEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLLM
human La         ICHQIEYYFGDFNLPRDKFLKEQI.KLDEGWVPLEIMIK
Xenopus LaA      ICEQIEYYFGDHNLPRDKFLKQQI.LLDDGWVPLETMIK
Drosophila La    ILRQMEYYFGDANLNRDKFLREQIGKNEDGWVPLSVLVT
S. c. Lhp1p      CLKQMEFYFSEFNFPYDRFLRTTAEK.NDGWVPISTIAT
```

FIGURE 19

```
   1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
  61 tagatttaat ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
 181 tatataagtt agggttaaga ttgacgatcc taagcaatat ctcgtgaacg tcactgcagc
 241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
 301 taaagcactt cttgaggtgg ctgagtctga tcctgagttc atctgctagt tggcagtcta
 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgttgt
 421 ccacaagaat actcaaccat tcatcgaaaa gtacttcaac aaagcagtac ttttgcctaa
 481 tgacttactg gaagtctgtg aatttgcata ggttctctat atttttgatg caactgaatt
 541 caaaaatttg tatcttgata ggatactttc ataagatatt cgtaaggaac tcactttccg
 601 taagtgttta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg
 661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa  .
 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
 781 ggcaataaag gaatctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga
 841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc
 901 catgaagaaa cacatgaagg cacctaaaat tcctaactct accttggaat caaagtactt
 961 gaccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
1021 gatccttggt aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgattc
1081 tgcatctgca cccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa
1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaat
1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc
1261 cggtgtttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt
1321 tgagaactcc aagatgttcc ctcttcaatt ctttagtgcc attgaagctg ttaatgaagc
1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaaag gtcaaatcga
1441 agcagtaaag gaagttgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
1501 aaccgaagaa ggagaatttg ttaaagtcaa cgaaggaatt ggcaagcaat acattaactc
1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca-aaggacacac
1621 tgcaatcttc tctgatgttt ctggttctat gagtacctca atgtcaggtg gagccaagaa
1681 gtatggttcc gttcgtactt gtctcgagtg tgcattagtc cttggtttga tggtaaaata
1741 acgttgtgaa aagtcctcat tctacatctt cagttcacct agttctcaat gcaataagtg
1801 ttactŧagaa gttgatctcc ctggagacga actccgtcct tctatgtaaa aactttŧgca
1861 agagaaagga aaacttggtg gtggtactga tttcccctat gagtgcattg atgaatggac
1921 aaagaataaa actcacgtag acaatatcgt tattttgtct gatatgatga ttgcagaagg
1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
2041 tgaagtaaat cctaacatta aaatctttgc agttgactta gaaggttacg gaaagtgcct
2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggta tgagcgattc
2161 aatcttaaag ttcatttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
2221 ctttgccctt caaaaaatag gacaaaagtg agtttcttga gattcttcta taacaaaaat
2281 ctcaccccac ttttttgttt tattgcatag ccattatgaa atttaaatta ttatctattt
2341 atttaagtta cttacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc
2401 aaagaacaaa aaagattaaa a
```

FIGURE 20

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL

VNVTAACLLQEGSYYQDKDERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTTN

YIVAFCVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS

QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTK

KKRKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKIAKRQNAMKKHMK

APKIPNSTLESKYLTFKDLIKFCHISEPKERVYKILGKKYPKTEEEYKAAFGDSASAP

FNPELAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGV

SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNLKGQIE

AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKIAVNKNLDEIKG

HTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ

CNKCYLEVDLPGDELRPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHVDNIVILSD

MMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFAVDLEGYGKCLNLGDEFNENNYI

KIFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK

FIGURE 21

```
   1 tcaatactat taattaataa ataaaaaaaa gcaaactaca aagaaaatgt caaggcgtaa
  61 ctaaaaaaag ccataggctc ctataggcaa tgaaacaaat cttgattttg tattacaaaa
 121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga
 181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga
 241 tgatgatgat gaagaaaaca actcaaataa ataataagaa ttattaagga gagtcaatta
 301 gattaagtag caagtttaat tgataaaaaa agttggttct aaggtagaga aagatttgaa
 361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta
 421 attaagaacg attactgaag aataggttaa gtattaaaat ttagtattta acatggacta
 481 ccagttagat ttaaatgaga gtggtggcca tagaagacac agaagagaaa cagattatga
 541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa tttacgccaa
 601 ctaaaagaca tcatattgtt ggtggcttaa agattatttt aataaaaaca attatgatca
 661 tcttaatgta agcattaaca gactagaaac tgaagccgaa ttctatgcct ttgatgattt
 721 ttcacaaaca atcaaactta ctaataattc ttactagact gttaacatag acgttaattt
 781 tgataataat ctctgtatac tcgcattgct tagatttta ttatcactag aaagattcaa
 841 tattttgaat ataagatctt cttatacaag aaattaatat aattttgaga aaattggtga
 901 gctacttgaa actatcttcg cagttgtctt ttctcatcgc cacttacaag gcattcattt
 961 acaagttcct tgcgaagcgt tctaatattt agttaactcc tcatcataaa ttagcgttaa
1021 agatagctaa ttataggtat actctttctc tacagactta aaattagttg acactaacaa
1081 agtccaagat tattttaagt tcttataaga attccctcgt ttgactcatg taagctagta
1141 ggctatccca gttagtgcta ctaacgctgt agagaacctc aatgttttac ttaaaaaggt
1201 caagcatgct aatcttaatt tagtttctat ccctacctaa ttcaattttg atttctactt
1261 tgttaattta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaca
1321 aaagcttgaa aatctacttt tgagtataaa ataatcaaaa aatcttaaat ttttaagatt
1381 aaacttttac acctacgttg cttaagaaac ctccagaaaa cagatattaa aacaagctac
1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaaagatga
1501 aactccaagc gaaagcacaa gtggtatgaa atttttgat catctttctg aattaaccga
1561 gcttgaagat ttcagcgtta acttgtaagc tacccaagaa atttatgata gcttgcacaa
1621 acttttgatt agatcaacaa atttaaagaa gttcaaatta agttacaaat atgaaatgga
1681 aaagagtaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct
1741 taaaagatgc tctgttaata tatcaaatcc tcatggaaac atttcttatg aactgacaaa
1801 taaagattct acttttata aatttaagct gaccttaaac taagaattat aacacgctaa
1861 gtatactttt aagtagaacg aattttaatt taataacgtt aaaagtgcaa aaattgaatc
1921 ttccicatta gaaagcttag aagatattga tagtctttgc aaatctattg cttcttgtaa
1981 aaatttacaa aatgttaata ttatcgccag tttgctctat cccaacaata tttagaaaaa
2041 tcctttcaat aagcccaatc ttctattttt caagcaattt gaataattga aaaatttgga
2101 aaatgtatct atcaactgta ttcttgatca gcatatactt aattctattt cagaattctt
2161 agaaaagaat aaaaaaataa aagcattcat tttgaaaaga tattatttat tacaatatta
2221 tcttgattat actaaaattat ttaaaacact tcaatagtta cctgaattaa attaagttta
2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa
2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaaac
2401 cctttagcta atagattttg accaaaacac tgtaagtgat gactctatta aaaagatttt
2461 agaatctata tctgagtcta agtatcatca ttatttgaga ttgaacccta gttaatctag
2521 cagtttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt gcgacgaaaa
2581 aggtgtttta gtaaaagcat actataaatt ccctctatgt ttaccaactg gtacttatta
2641 cgattacaat tcagatagat ggtgattaat taaatattag tttaaataaa tattaaatat
2701 tgaatatttc tttgcttatt atttgaataa tacatacaat agtcattttt agtgttttga
2761 atatattta gttatttaat tcattatttt aagtaaataa ttattttca atcattttt
2821 aaaaaatcg
```

FIGURE 22

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQIK

EEDLKLLKFKNQDQDGNSGNDDDDEENNSNKQQELLRRVNQIKQQVQLIKKVGSKVEK

DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR

ETDYDTEKWFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNYDHLNVSINRLETEAE

FYAFDDFSQTIKLTNNSYQTVNIDVNFDNNLCILALLRFLLSLERFNILNIRSSYTRN

QYNFEKIGELLETIFAVVFSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF

STDLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL

VSIPTQFNFDFYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNLKFLRLNFYTY

VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED

FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLK

RCSVNISNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSAKIE

SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNLLFFKQFEQLK

NLENVSINCILDQHILNSISEFLEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPE

LNQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFDQNTVSD

DSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP

LCLPTGTYYDYNSDRW

FIGURE 23

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL

PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKIARNEDVNNSLFCHS

ANVNVTLLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK

WVQRSSSSSATAAQIKQLTEPVTNKQFLHKLNINSSSFFPYSKILPSSSSIKKLTDLR

EAIFPTNLVKIPQRLKVRINLTLQKLLKRHKRLNYVSILNSICPPLEGTVLDLSHLSR

QSPKERVLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLLSLPLNGYLPFDSLLKKL

RLKDFRWLFISDIWFTKHNFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVTI

VYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLSNFNHSKMRIIPKKSNNEFR

IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE

FKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN

TNTGVLKLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY

IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV

INIKKLAMGGFQKYNAKANRDKILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN

NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF

KDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIEYEVRFTILNGFLESLSSNTS

KFKDNIILLRKEIQHLQAYIYIYIHIVN

FIGURE 24

Oxytricha   LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Euplotes   LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIGURE 25

```
                                          Motif 0
human         AKFLHWLMSVYVVELLRSFFYVTETTFQKNR
tez1     ISEIEWLVLGKRSNAXMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNR
EST2     LKDFRWLFISD---IWFTKHNFENLNQLAICFISWLPRQLIPKIIQTFFYCTEISSTVT-
p123     TREISWMQVET-SAXHPYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK
                              .  *.      .     ....*** **


                                          Motif 1
human     LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKP--DGL
tez1      TVYFRKDIWKLLCRPFI-TSMKMEAFEKINENNVRMDTQK-TTLPPAVIRLLPKK--NTF
EST2      IVYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLS--NFNHSKMRIIPKKSNNEF
p123      TYYYRKNIWDVIMKMSI-ADLKKETLAEVQEKEVEEWKKS-LGFAPGKLRLIPKK--TTF
            ..*.  *   .     *     *              .*  .**

Motif 2
human     RPIVNHDYVVGARTFRREKRAERLTSRVKALF-SVLNYERA
tez1      RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFHLEVYMKLLTF
EST2      RIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF
p123      RPIMTFNKKIVNSDRKTTXLTTNTKLLNSHLMLKTLKN-RMFKDPPGFAVFNYDDVMKKY
            *  *              *                  *

                    Motif 3 (A)
tez1      KKDLLKHRMFGR-KKYFVRIDIKSCYDRIKQDLMFRIVKR-KLKDPEPVIRKYATIHATS
EST2      KQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFFNTN
p123      EEFVCKWKQVGQPKLPFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFHIHTAQILKRKN
            . *       .*   *   ***  .         .*    *
```

FIGURE 26

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT
TCTAACTACGTGTTTCGCACTACCAAATTCAAGAAAAATAGCATTACCATGCCTTCCTGG
TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG
TCTTTTTTGCCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGGAAAAT
GTTCCACAGTTTGGTCGGTACATACGCATTCGTTGATTTATTGATCAATTATACAGTAAT
TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT
GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
ACTTACAGAACCAGTGACAAATAAACAATTCTTACACAAGCTCAATATAAATTCCTCTTC
TTTTTTTCCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT
GAGAGAAGCTATTTTTCCCACAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT
TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT
GAATAGTATTTGCCCACCATTGGAAGGGACCGTATTGGACTTGTCGCATTTGAGTAGGCA
ATCACCAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAGTTATTACCCCA
AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTATCAAGAATCTAAATCTTTTATT
AAGTTTACCCTTAAATGGCTATTTACCATTTGATAGTTTGTTGAAAAAGTTAAGATTAAA
GGATTTTCGGTGGTTGTTCATTTCTGATATTTGGTTCACCAAGCACAATTTTGAAAACTT
GAATCAATTGGCGATTTGTTTCATTTCCTGGCTATTTAGACAACTAATTCCCAAAATTAT
ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA
TGATACTTGGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTACTTAGT
CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA
AATGAGGATTATACCAAAAAAAAGTAATAATGAGTTCAGGATTATTGCCATCCCATGCAG
AGGGGCAGACGAAGAAGAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC
CACTCAAAAAATTTTAGAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA
TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAATT
TAATAATGTCTTACCAGAGCTTTATTTCATGAAATTTGATGTCAAATCTTGCTATGATTC
CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGTT
TTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT
TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAACAGCTTT
GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTCAGGGCTCTAGTTTATC
TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC
CAGTCCTAGCCAGGACACATTAATTTTAAAACTGGCTGACGATTTCCTTATAATATCAAC
AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA
TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT
TATTCAATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAAACATTCAAG
CACAATGAATAATTTCCATATCCGTTCGAAATCTAGTAAAGGGATATTTCGAAGTTTAAT
AGCGCTGTTTAACACTAGAATCTCTTATAAAACAATTGACACAAATTTAAATTCAACAAA
CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTCGGAATGTTATAAATCTGC
TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTCATTCGTTCTTACAACG
CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA
TGAGGTACGATTCACCATATTGAATGGATTTTTGGAAAGCCTATCTTCAAACACATCAAA
ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCAACACTTGCAAGC

FIGURE 27

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR
AERLTSRVKALFSVLNYERA

FIGURE 28

```
GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC
TTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAA
GAGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGA
AGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACG
GGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCG
CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGC
GTGCTCAACTACGAGCGGGCGCG
```

FIGURE 29

MTEHHTPKSRILRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHEDFRAMHVNGVQNDLV
STFPNYLISILESKNWQLLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRK
RTIETSITQNKSARKEVSWNSISISRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMWLQWIFPRQFG
LINAFQVKQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEIEWLVL
GKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFIT
SMKMEAFEKINENNVRMDTQKTTLPPAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTNQT
LRPVASILKHLINEESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLMFR
IVKKKLKDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKVVQLLSMKTSDTLFVDFVDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENSNGIINNTFFNESKKRMPFFG
FSVNMRSLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCNI
YRLGYSMCMRAQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFC
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLFLHRRJAD

FIGURE 30·

ggtaccgatttactttccttttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatattttttacaagaactcaataacaataccaagtcaaattccaatatgaagg

tgttattagtgatcgataatatttctattttatcggtcgttaccaagtataaggacaaaaagaacaacttccttcccccctaaagactttttactttattaatttacttttcaaatatatttcg

ggttcgcttactttttaatcgtggtactgtttagctgctacttctagccaaccgcgtgtttctaccccgtcattggatatagctcttggagtagctcacagaaatccttacaaatctt

ctgatgagactatattagattcattacagtccgtgcatattcttaacatggagccttacactttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttg

aaaaggttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagttttttgatgcttgcacacgtctagcatgattgagatattcaaaaatttctatccactacaa

ctcctttaacgcggtttattttctatttctattctcatgttgttccaaatatgtatcatctcgtattaggcttttttccgtttttactcctggaatcgtaccttttcactattccccctaatg

aataatctaaattagtttcgcttataattgatagtagtagaaagattggtgattctactcgtgtaatgttattagtttaaagatactttgcaaaacatttattagctatcattatataaaa

aaaatcctataattataaatattaatcaatatttgcggtcactatttatttaaaacgttatgatcagtaggacactttgcatatatatagttatgcttaatggttacttgtaacttgcAT

GACCGAACACCATACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTA

CCTTAAATGATTATGTACAACTTGTTTTGAGAGGGTCGCCGGCAAGCTCGTATAGCAATATATGCGAA

CGCTTGAGAAGCGATGTACAAACGTCCTTTTCTATTTTTCTTCATTCGACTGTAGTCGGCTTCGACAGT

AAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAAATGCTCACAGTCAGAGgtatatatattttgttttgatttttttctattcg

ggatagctaatatatgggcagCTAATAGCGAATGTTGTAAAACAGATGTTCGATGAAAGTTTTGAGCGTCGAAGGA

ATCTACTGATGAAAGGGTTTTCCATGgtaaggtattctaattgtgaaatatttacctgcaattactgtttcaaagagattgtatttaaccgataaagAA

TCATGAAGATTTTCGAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCCTAATTA

CCTTATATCTATACTTGAGTCAAAAAATTGGCAACTTTTGTTAGAAATgtaaataccggttaagatgttgcgcactttgaaca

agactgacaagtatagTATCGGCAGTGATGCCATGCATTACTTATTATCCAAAGGAAGTATTTTTGAGGCTCTTC

CAAATGACAATTACCTTCAGATTTCTGGCATACCACTTTTTAAAAATAATGTGTTTGAGGAAACTGTGT

CAAAAAAAAGAAAGCGAACCATTGAAACATCCATTACTCAAAATAAAAGCGCCCGCAAAGAAGTTTC

CTGGAATAGCATTTCAATTAGTAGGTTTAGCATTTTTTTACAGGTCATCCTATAAGAAGTTTAAGCAAGgt

aactaatactgttatccttcataactaattttagATCTATATTTTAACTTACACTCTATTTGTGATCGGAACACAGTACACATG

TGGCTTCAATGGATTTTTTCCAAGGCAATTTGGACTTATAAACGCATTTCAAGTGAAGCAATTGCACAA

AGTGATTCCACTGGTATCACAGAGTACAGTTGTGCCCAAACGTCTCCTAAAGGTATACCCTTTAATTGA

ACAAACAGCAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTATTGCCCATATATTGA

CACCCACGATGATGAAAAAATCCTTAGTTATTCCTTAAAGCCGAACCAGGTGTTTGCGTTTCTTCGATC

CATTCTTGTTCGAGTGTTTCCTAAATTAATCTGGGGTAACCAAAGGATATTTGAGATAATATTAAAAGg

tattgtataaaatttattaccactaacgattttaccagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTAC

ATTATTTAATGAGTAACATAAAGgtaatatgccaaattttttttaccattaattaacaatcagATTTCAGAAATTGAATGGCTAGT

CCTTGGAAAAAGGTCAAATGCGAAAATGTGCTTAAGTGATTTTGAGAAACGCAAGCAAATATTTGCGG

AATTCATCTACTGGCTATACAATTCGTTTATAATACCTATTTTACAATCTTTTTTTTATATCACTGAATC

AAGTGATTTACGAAATCGAACTGTTTATTTTAGAAAAGATATTTGGAAACTCTTGTGCCGACCCTTTAT

TACATCAATGAAAATGGAAGCGTTTGAAAAAAATAAACGAGgtatttaaagtattttttgcaaaaagctaatatttcagAACAA

TGTTAGGATGGATACTCAGAAAACTACTTTGCCTCCAGCAGTTATTCGTCTATTACCTAAGAAGAATAC

CTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAGgtattaatttttggtcatcaatgtactttacttctaatctattattag

cagATGGGTTCAAACAAAAAAATGTTAGTCAGTACGAACCAAACTTTACGACCTGTGGCATCGATACTG

AAACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTAACTTGGAGGTTTACATGAAGCTTCTTACT

TTTAAGAAGGATCTTCTTAAGCACCGAATGTTTGGtaattatataatgcgcgattcctcattattaattttgcagGCGTAAGAAG

TATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATTGTT

AAAAAGAAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATACATGCAACAAGTGACCG

AGCTACAAAAAACTTTGTTAGTGAGGCGTTTTCCTATTgtaagtttatttttttcattggaattttttaacaaattcttttttagTTGATAT

GGTGCCTTTTGAAAAAGTCGTGCAGTTACTTTCTATGAAAACATCAGATACTTTGTTTGTTGATTTTGT

GGATTATTGGACCAAAAGTTCTTCTGAAATTTTTAAAATGCTCAAGGAACATCTCTCTGGACACATTGT

TAAGgtataccaattgttgaattgtaataacactaatgaaactagATAGGAAATTCTCAATACCTTCAAAAAGTTGGTATCCCTC

AGGGCTCAATTCTGTCATCTTTTTTGTGTCATTTCTATATGGAAGATTTGATTGATGAATACCTATCGTT

TACGAAAAAGAAAGGATCAGTGTTGTTACGAGTAGTCGACGATTTCCTCTTTATAACAGTTAATAAAA

AGGATGCAAAAAAATTTTTGAATTTATCTTTAAGAGgtgagttgctgtcattcctaagttctaaccgttgaagGATTTGAGAA

ACACAATTTTTCTACGAGCCTGGAGAAAACAGTAATAAACTTTGAAAATAGTAATGGGATAATAAACA

ATACTTTTTTTAATGAAAGCAAGAAAGAATGCCATTCTTCGGTTTCTCTGTGAACATGAGGTCTCTTG

ATACATTGTTAGCATGTCCTAAAATTGATGAAGCCTTATTTAACTCTACATCTGTAGAGCTGACGAAAC

ATATGGGGAAATCTTTTTTTTTACAAAATTCTAAGgtatactgtgtaactgaataatagctgacaaataatcagATCGAGCCTTGC

ATCCTTTGCACAAGTATTTATTGACATTACCCACAATTCAAAATTCAATTCTTGCTGCAATATATATAG

GCTAGGATACTCTATGTGTATGAGAGCACAAGCATACTTAAAAAGGATGAAGGATATATTTATTCCCC

AAAGAATGTTCATAACGGgtgagtacttattttaactagaaaagtcattaattaaccttagATCTTTTGAATGTTATTGGAAGAAAA

ATTTGGAAAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTTGTCCTCTGCAGAAGTCAA

FIGURE 30 (cont.)

ATGgtacgtgtcggtctcgagacttcagcaatattgacacatcagGCTTTTTTGTCTTGGAATGAGAGATGGTTTGAAACCCTCTT
TCAAATATCATCCATGCTTCGAACAGCTAATATACCAATTTCAGTCATTGACTGATCTTATCAAGCCGC
TAAGACCAGTTTTGCGACAGGTGTTATTTTTACATAGAAGAATAGCTGATTAAtgtcattttcaatttattatatacatcctt
tattactggtgtcttaaacaatattattactaagtatagctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagttttgattgacttgtcttt
atccttatactttaagaaagattgacagtggttgctgactactgcccacatgcccattaaacgggagtggttaaacattaaaagtaatacatgaggctaatctcctttcatttag
aataaggaaagtggttttctataatgaataatgcccgcactaatgcaaaaagacgaagattatcttctaaacaaggggggattaagcatatccgaaggaaaagagagtaatat
acccagtgttgttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagccccaggttatccatggtggccg
gccttgctactgagacgaaaagaaactaaggatagtttgaatactaatagctcatttaatgtcttatataaggttttgttttttcctgacttcaattttgcatgggtgaaaagaaata
gtgttaagccattattggattccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcctcctgatttaaaggag
gaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaattttttgcaaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcgga
gagtatctccagcggatccttgatgtcaataacttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaaggtacc

FIGURE 31

```
EST2 pep            FFYCTEISST VTIVYFRHDT WN----KLIT P-----FIVE YFK-TYLVEN    40
Euplotes pep        FFYVTEQQKS YSKTYYYRKN IWDVI-MKMS IAD----LKK ETLA--EVQE    43
Trans of tetrahymen ------KHKE GSQIFYYRKP IWKLVSKLTI VKVRIQFSEK NKQMKNNFYQ    44

Consensus           FFY.TE..K. .S..YYYRK. IW...-KL.. ...----F..K .......V..    50


EST2 pep            NVCRNHNSY- ---------- TLSNFNHSKM RLIPKKSNNE FRLIAIPCRG    79
Euplotes pep        KEVEEWKKSL ---------- ---GFAPGKL RLIPKKIT-- FRFIMTFNKK    78
Trans of tetrahymen KIQLEEENLE KVEEKLIPED SFQKYPQGKL RLIPKKGS-- FRFIMTFLRK    92

Consensus           K...E..... ---------- ....F..GKL RLIPKK.--  FRFIMTF.RK   100


EST2 pep            ADEEEFTIYK ENHKNAIQPT QKILEYLRNK RPTSFTKIYS PTQIADRIKE   129
Euplotes pep        IVNSDRKTTK LTTNTKLLNS HLMLKTLKN- ------RMFK -DPFGFAVFN   120
Trans of tetrahymen DKQKNIK--- LNLNQILMDS QLVFRNLKD- ------ML-G -QKIGYSVFD   130

Consensus           ......K..K LN.N..L..S QL.L..LKN- ------.... -..IG..VF.   150


EST2 pep            FKQRLLKKFN NVL------- -PELYFMKFD VKSCYD                 157
Euplotes pep        YD-DVMKKYE EFVCKWKQVG QKLFFATMD IEKCYD                  155
Trans of tetrahymen NK-QISEKFA QFIEKWKNKG RPLEYYVTL- ------                 158

Consensus           .K-...KKF. .F..KWK..G .ELEYF.T.D ...CYD                 186
```

FIGURE 32

S-1: FFY VTE TTF QKN RLF FYR KSV WSK
S-2: RQH LKR VQL RDV SEA EVR QHR EA
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q .
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

FIGURE 33

FIGURE 34

```
Poly 4
             t        t        c
     t a     a   g    c   c    t c g
5'- cag acc aaa gga att cca taa gg -3'
     Q   T   K   G   I   P   Q   G
```

4 (B')

5 (c')

```
     D   D   Y   L   L   I   T
3'- ctg ctg atg gag gag tag tgg -5'
     a   a   a a a a a   a   a
                 t   t   t   t
                     c   c
                    Poly 1
```

FIGURE 35

622 —

309 —

160 —

T
M1
M2

B
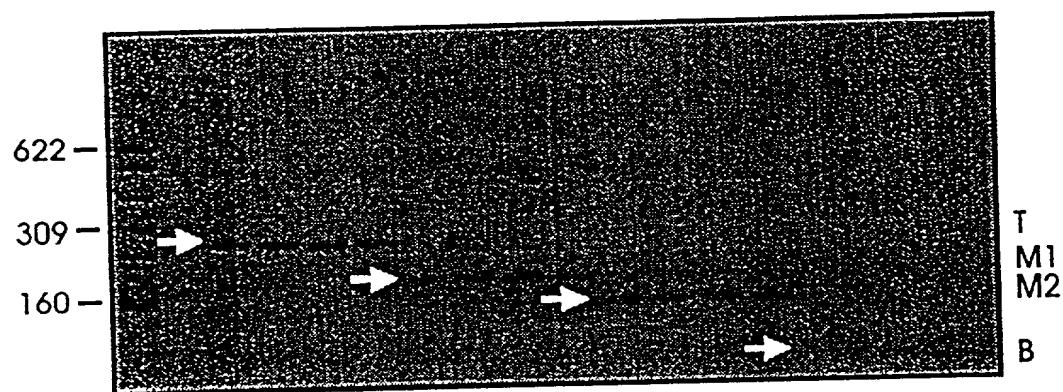
Motif B' (4)

QTKGIP**QG**

Motif C (5)

DDYLLIT

FIGURE 36

PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

```
Ot              LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123    KGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2                SILSSFLCHFYMEDLIDEYLSFTKKK--------GSVLLRVV
Sc_p103    DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS------QDTLILKLADDFLIIS
                     .*  .        * .     *              . ... . .


Q    K    V    G    I    P    Q    G
caa  aaa  gtt  ggt  atc  cct  cag  gg......    <---Actual Genomic Sequence.


Poly 4
          t         t         c
t    a    a    g    c    c    t c g
cag  acc  aaa  gga  att  cca  taa  gg ---->


ag  acc  aaa  gga  att  cca  tca  ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
tc  tgg  ttt  cct  taa  ggt  agt  ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

          K    G    I    P    S    G   S   I   L   S   S   F   L   C   H   F   Y   M



GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E   D   L   I   D   E   Y   L   S   F   T   K   K   K   G   S   V   L   L   R



GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg

V   V   D   D   Y   L   L   I   T


   <---- ctg ctg atg gag gag tag tgg
         a   a   a a a a a   a   a
                 t   t   t   t
                 c   c
                 Poly 1


.....gac gat ttc ctc ttt ata aca......    <---Actual Genomic Sequence.
     D   D   F   L   F   I   T
```

FIGURE 37

3' RT PCR Strategy

mRNA

Q_T

5'

Q_O

3'

Q_I
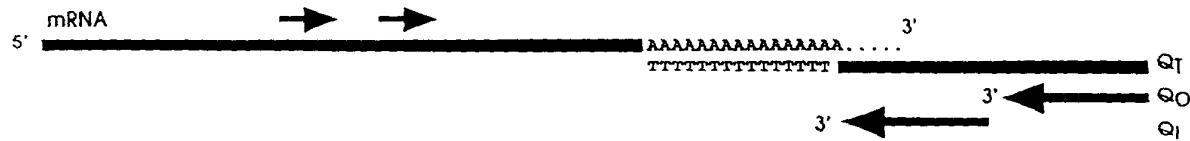
1. Synthesis of cDNA with Q_T Primer.

mRNA

Q_T

5'

3'

5'
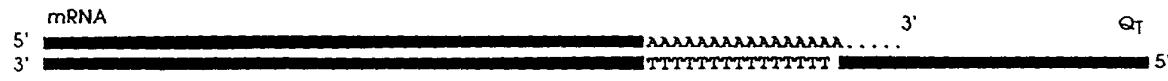
2. First Round PCR Using Outside Primer and Q_O Primer.

3'

Q_O
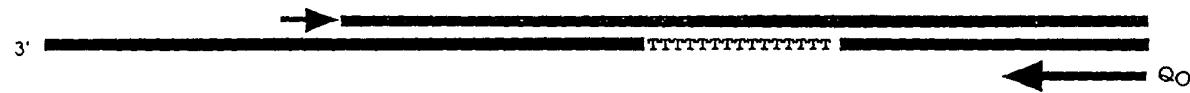
3. Second Round PCR Using Inside Primer and Q_I Primer.

Q_I
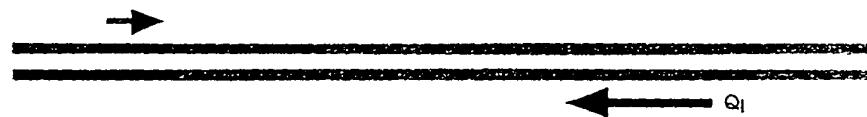
4. Sequence Second Round PCR Products Using Inside Primer or Q_I Primer.

FIGURE 38

A
-Size Selected Libraries from P. Nurese
    3 ~ 4 kb
    5 ~ 6 kb
    7 ~ 8 kb
    11 ~ 12 kb

-Libraries from J.A. Wise
    Sau 3a Partial Digest
    Hind III Partial Digest

cDNA Libraries

    GAD (Gal Activation Domain) Library
    REP Library from R. Allshire
    REP81ES Library (old)
    REP81ES Library (new)
    REP41ES Library

B.

Original PCR
3' RT-PCR

500 bp

C

—603
—310
—234
—194

D.

Mg Conc.

603—
310—
234—
194—

FIGURE 39

A5 B2

23K—
9.4K—
6.5K—

2.3K—
2K—

Hind III Digested Positive Genomic Clones
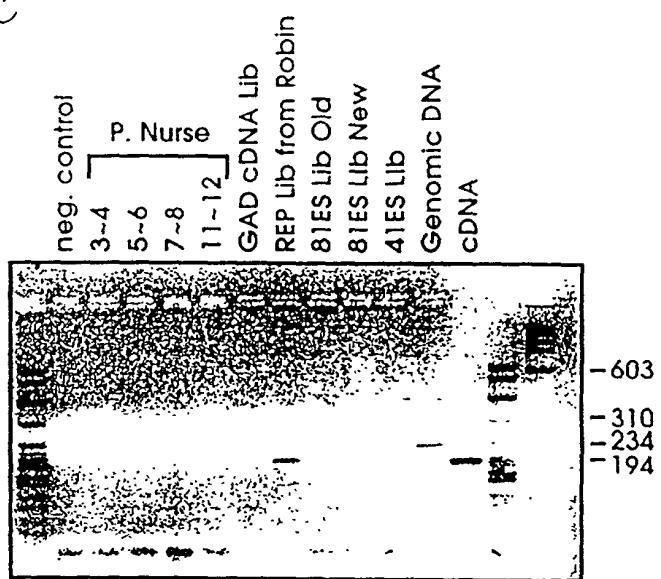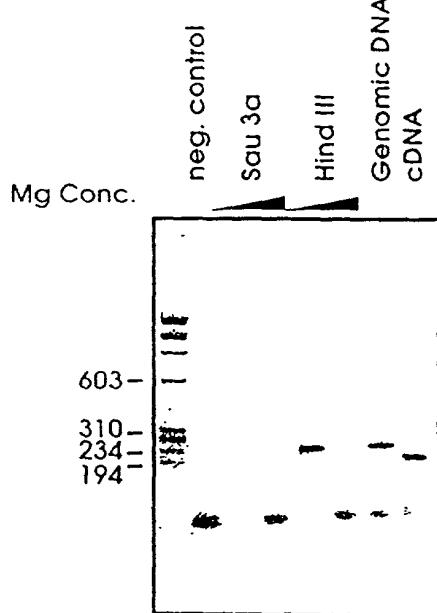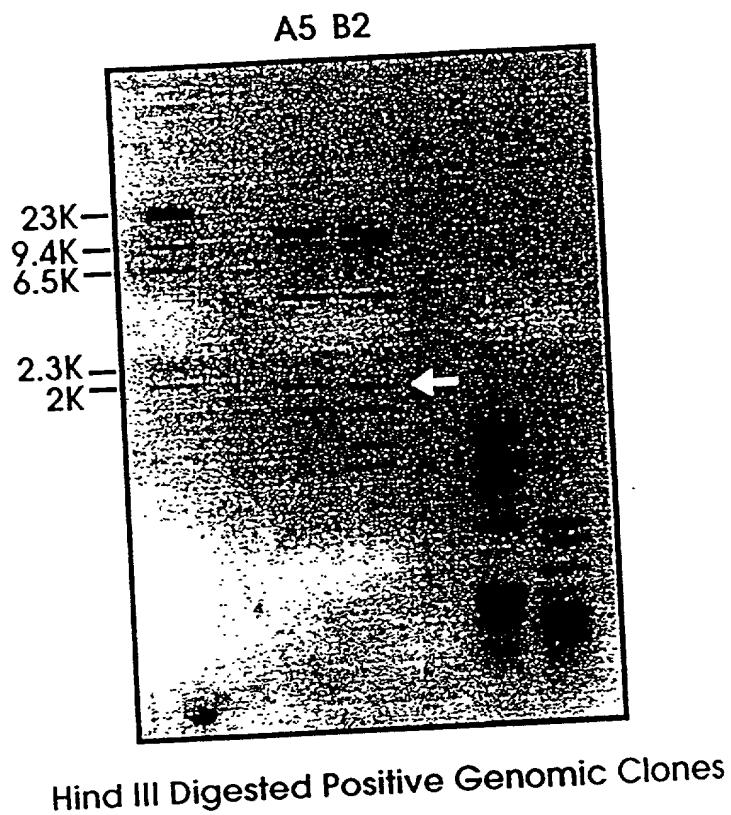
FIGURE 40

5' RT PCR Strategy
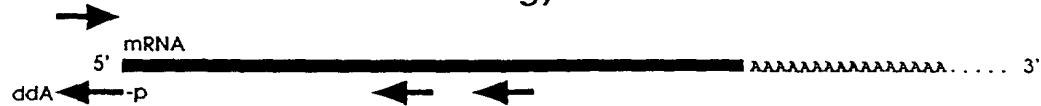
1. Synthesis of cDNA with Specific Downstream Primer.
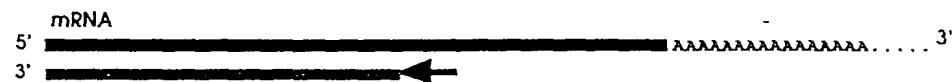
2. Ligate Oligo with 5'-P and blocked 3' to cDNA using T4 RNA Ligase.
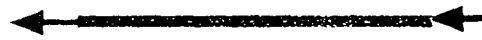
3. First Round PCR
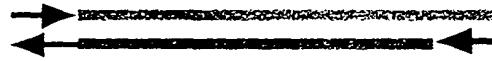
4. Second Round PCR
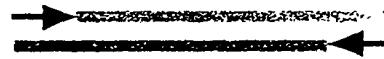
FIGURE 41

Alignment of RT Domains from Telomerase Catalytic Subunits.

```
                                Motif O
S.p. Tez1p (429).  WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIW ...(35)...
S.c. Est2p (366).  WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ...(35)...
E.a. p123  (441).  WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW ...(35)...
                    *           *** **              *  *     *

           Motif 1      Motif 2     K
           p hh h K      hR h        R
S.p. Tez1p AVIRLLPKK--NTFRLITN-LRKRF ...(61)...
S.c. Est2p SKMRIIPKKSNNEFRIIAIPCRGAD ...(62)...
E.a. p123  GKLRLIPKK--TTFRPIMTFNKKIV ...(61)...
               *   ***       ** *

           Motif 3(A)  AF
              h  hDh   GY  h
S.p. Tez1p KKYFVRIDIKSCYDRIKQDLMFRIVK ...(89)...
S.c. Est2p ELYFMKFDVKSCYDSIPRMECMRILK ...(75)...
E.a. p123  KLFFATMDIEKCYDSVNREKLSTFLK ...(107)...
              *     *   ***              *

           Motif 4(B')
               hPQG    pP hh    h
S.p. Tez1p YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ...(6)...
S.c. Est2p YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF ...(8)...
E.a. p123  YKQTKGIPQGLCVSSILSSFYYATLEESSLGF ...(14)...
             *      *   **    *            *        *

              Y Motif 5(C)                     Motif 6(D)
              h  F  DDhhh                       Gh h  cK  h
S.p. Tez1p VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENS .(205)
S.c. Est2p LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQS .(173)
E.a. p123  LLMRLTDDYLLITTQENNAVLFIEKLINVSRENGFKFNMKKLQTSFPLS .(209)
              **  *  *                          *          *
```

FIGURE 42

FIGURE 43

Disruption strategy for the putative telomerase genes.

wild type telomerase gene

wild type telomerase gene

1. Transform with linear fragment containing the telomerase gene disrupted with a *LEU2* or *ura4* marker.

M

telomerase gene::M

wild type telomerase gene

2. Assay in selective media.

3. Sporulate, and grow on selective media.

wild type telomerase gene

Wild Type (X2)

M

telomerase gene::M
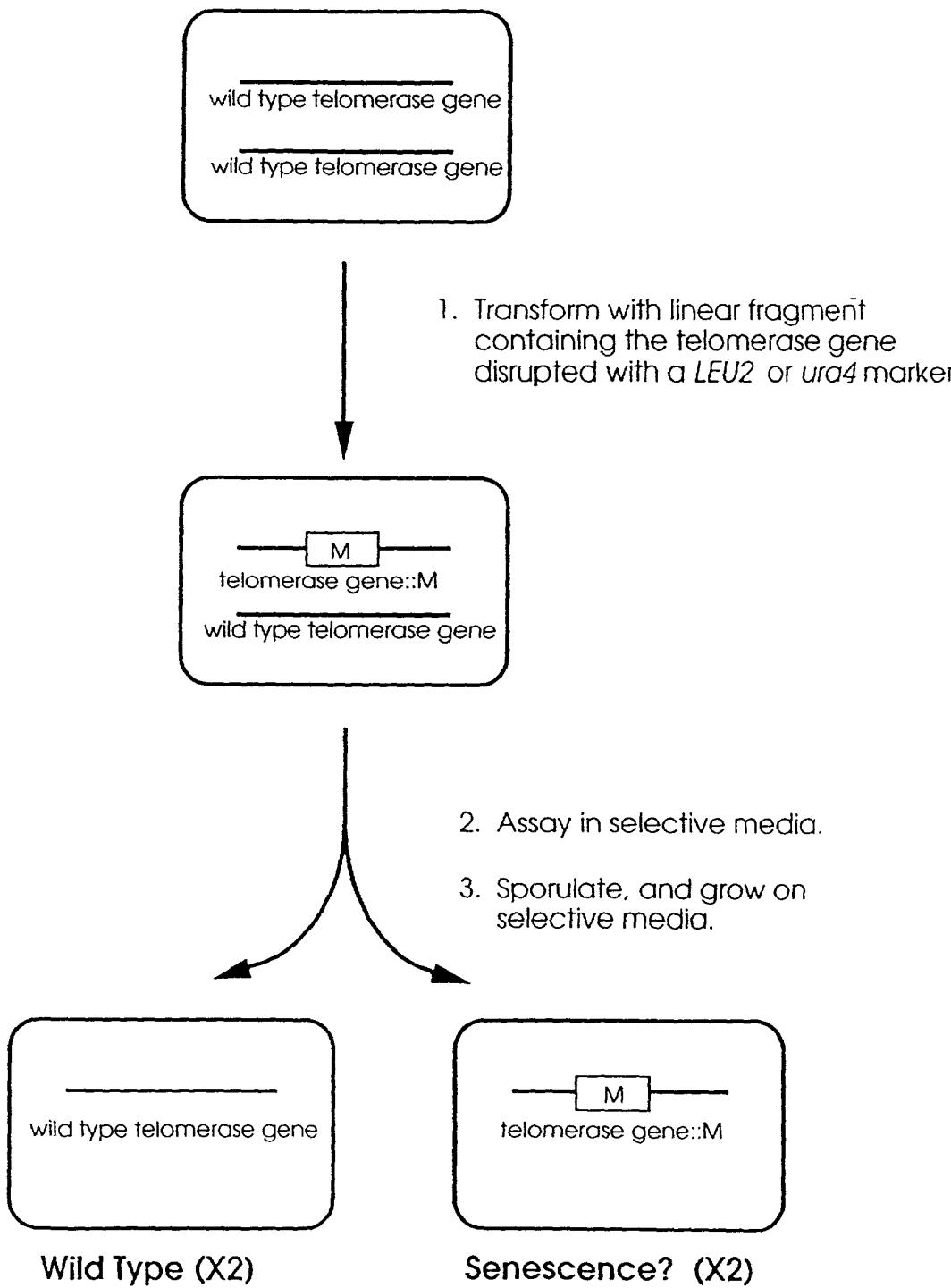
Senescence? (X2)

(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIGURE 44

An Example of Confirmation of tez1 disruption By PCR
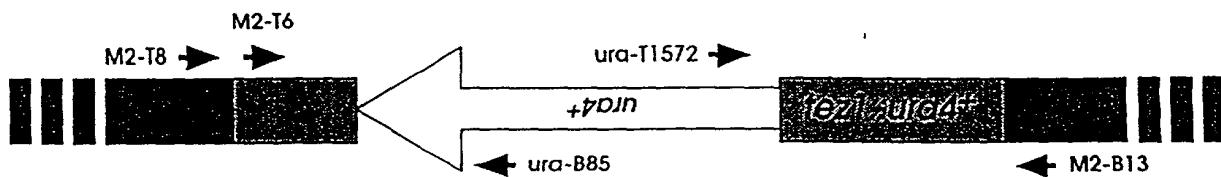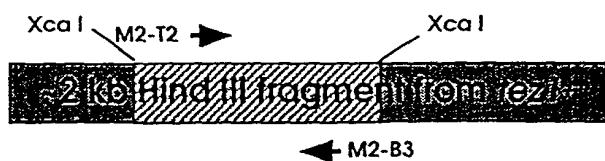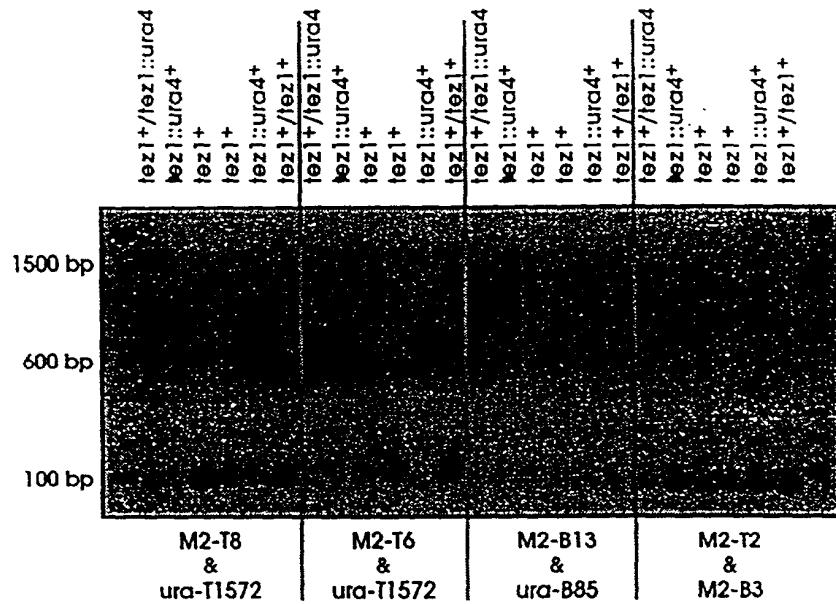
FIGURE 45

Tez1 disruption causes progressive
shortening of telomeres in *S. pombe*
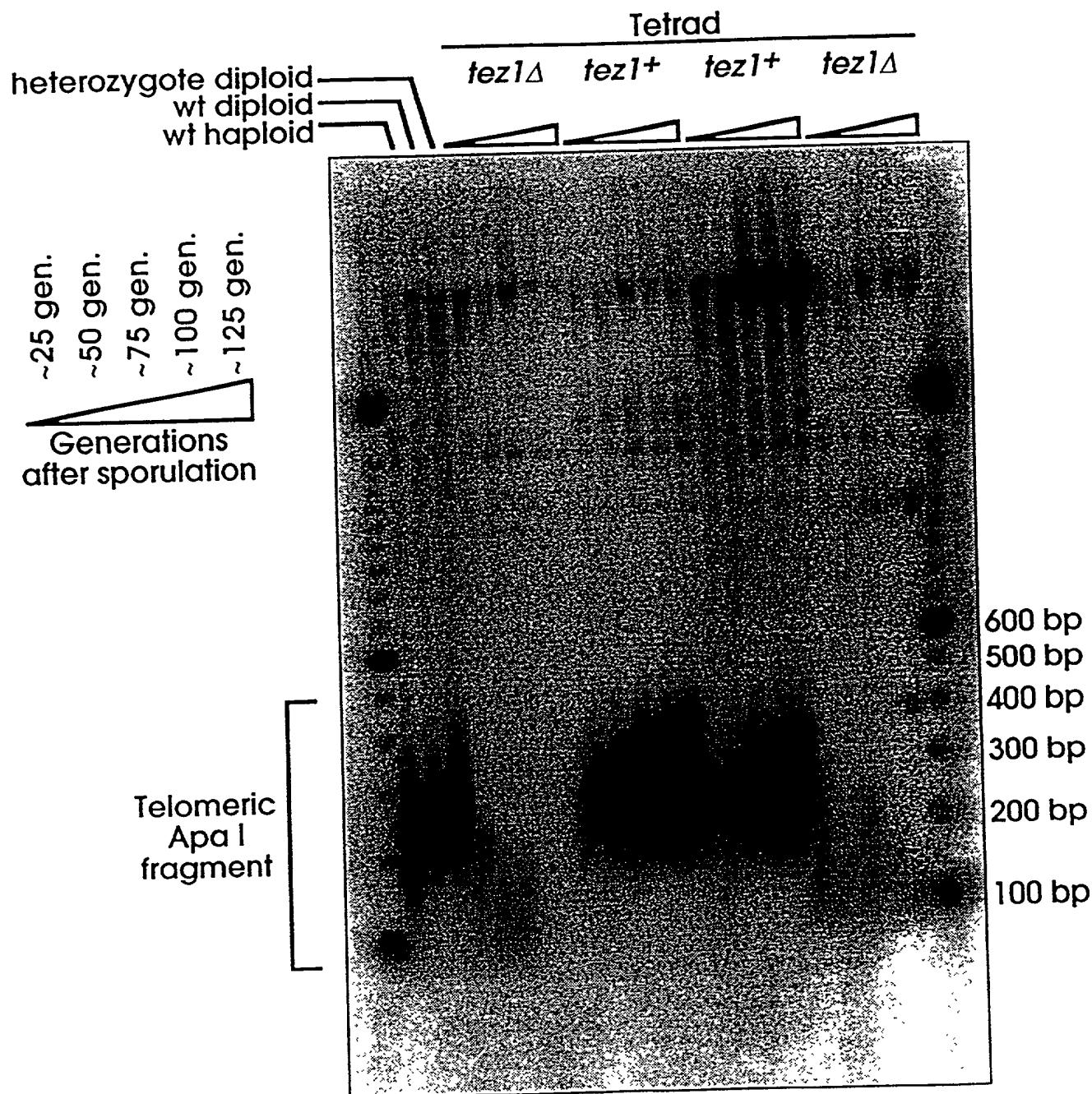
FIGURE 46

```
1   ggtaccgatttactttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatattttacaaga 80
81  actcaataacaataccaagtcaaattccaatatgaaggtgttattagtgatcgataatatttctattttatcggtcgtta 160
161 ccaagtataaggacaaaaagaacaacttccttccccctaaagactttttactttattaatttacttttcaaatatatttcg 240
241 ggttcgcttacttttaatcgtggtactgttttagctgctacttctagccaaccgcgtgtttctacccgtcattggatat 320
321 agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtccgtgcatattc 400
401 ttaacatggagccttacactttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttgaaaag 480
481 gttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagttttttgatgcttgcacacgtctagcatg 560
561 attgagatattcaaaaatttctatccactacaactcctttaacgcggtttttatttttctattttctattctcatgttgtt 640
641 ccaaatatgtatcatctcgtattaggctttttttccgtttttactcctggaatcgtacctttttcactattcccctaatga 720
721 ataatctaaaattagtttcgcttataattgatagtagtagaaagattggtgattctactcgtgtaatgttattagtttaaa 800
801 gatactttgcaaaacatttattagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc 880
881 actatttatttaaaacgttatgatcagtaggacactttgcatatatatagttatgcttaatggttacttgtaacttgc    958
```

```
959  ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018
1    M   T   E   H   H   T   P   K   S   R   I   L   R   F   L   E   N   Q   Y   V  20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078
21   Y   L   C   T   L   N   D   Y   V   Q   L   V   L   R   G   S   P   A   S   S  40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT 1138
41   Y   S   N   I   C   E   R   L   R   S   D   V   Q   T   S   F   S   I   F   L  60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
61   H   S   T   V   V   G   F   D   S   K   P   D   E   G   V   Q   F   S   S   P  80
```

FIGURE 46 (cont.)

```
1199 AAA TGC TCA CAG TCA GAG gtatatatattttttgttttgattttttttctattcgggatagctaatatatgggcag 1272
  81 K   C   S   Q   S   E                                                             86

1273 CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA 1332
  87 L   I   A   N   V   V   K   Q   M   F   D   E   S   F   E   R   R   R   N   L  106

1333 CTG ATG AAA GGG TTT TCC ATG gtaaggtattctaattgtgaaatatttacctgcaattactgtttcaaagaga 1405
 107 L   M   K   G   F   S   M                                                        113

1406 ttgtatttaaccgataaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT 1469
 114                     N   H   E   D   F   R   A   M   H   V   N   G   V   Q   N  128

1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529
 129 D   L   V   S   T   F   P   N   Y   L   I   S   I   L   E   S   K   N   W   Q  148

1530 CTT TTG TTA GAA AT gtaaataccggttaagatgttgcgcactttgaacaagactgacaagtatag T ATC GGC 1601
 149 L   L   L   E   I                                                        I   G  155

1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661
 156 S   D   A   M   H   Y   L   L   S   K   G   S   I   F   E   A   L   P   N   D  175

1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721
 176 N   Y   L   Q   I   S   G   I   P   L   F   K   N   N   V   F   E   E   T   V  195

1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA 1781
 196 S   K   K   R   K   R   T   I   E   T   S   I   T   Q   N   K   S   A   R   K  215

1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841
 216 E   V   S   W   N   S   I   S   I   S   R   F   S   I   F   Y   R   S   S   Y  235

1842 AAG AAG TTT AAG CAA G gtaactaatactgttatccttcataactaattttag AT CTA TAT TTT AAC
1907
 236 K   K   F   K   Q   D                                             L   Y   F   N  245

1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967
 246 L   H   S   I   C   D   R   N   T   V   H   M   W   L   Q   W   I   F   P   R  265

1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2027
 266 Q   F   G   L   I   N   A   F   Q   V   K   Q   L   H   K   V   I   P   L   V  285

2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087
 286 S   Q   S   T   V   V   P   K   R   L   L   K   V   Y   P   L   I   E   Q   T  305

2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147
 306 A   K   R   L   H   R   I   S   L   S   K   V   Y   N   H   Y   C   P   Y   I  325

2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207
 326 D   T   H   D   D   E   K   I   L   S   Y   S   L   K   P   N   Q   V   F   A  345

2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA 2267
 346 F   L   R   S   I   L   V   R   V   F   P   K   L   I   W   G   N   Q   R   I  365

2268 TTT GAG ATA ATA TTA AAA G gtattgtataaaatttattaccactaacgattttaccag AC CTC GAA ACT 2336
 366 F   E   I   I   L   K   D                                             L   E   T  375
```

FIGURE 46 (cont.)

```
2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG 2396
376  F   L   K   L   S   R   Y   E   S   F   S   L   H   Y   L   M   S   N   I   K   395

2397 gtaatatgccaaattttttttaccattaattaacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA 2465
396                                           I   S   E   I   E   W   L   V   L   G   405

2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG 2525
406  K   R   S   N   A   K   M   C   L   S   D   F   E   K   R   K   Q   I   F   A   425

2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT 2585
426  E   F   I   Y   W   L   Y   N   S   F   I   I   P   I   L   Q   S   F   F   Y   445

2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA 2645
446  I   T   E   S   S   D   L   R   N   R   T   V   Y   F   R   K   D   I   W   K   465

2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA-ATA AAC GAG 2705
466  L   L   C   R   P   F   I   T   S   M   K   M   E   A   F   E   K   I   N   E   485

2706 gtattttaaagtattttttgcaaaaagctaatattttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775
486                                           N   N   V   R   M   D   T   Q   K   T   495

2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG 2835
496  T   L   P   P   A   V   I   R   L   L   P   K   K   N   T   F   R   L   I   T   515

2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtattaattttggtcatcaatgtactttacttctaatctatta 2906
516  N   L   R   K   R   F   L   I   K                                               524

2907 ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG 2967
525          M   G   S   N   K   K   M   L   V   S   T   N   Q   T   L   R   P   V   542

2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG 3027
543  A   S   I   L   K   H   L   I   N   E   E   S   S   G   I   P   F   N   L   E   562

3028 GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat 3088
563  V   Y   M   K   L   L   T   F   K   K   D   L   L   K   H   R   M   F   G      581

3089 tatataatgcgcgattcctcattattaattttgcag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA 3155
582                                         R   K   K   Y   F   V   R   I   D   I   591

3156 AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC 3215
592  K   S   C   Y   D   R   I   K   Q   D   L   M   F   R   I   V   K   K   K   L   611

3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT 3275
612  K   D   P   E   F   V   I   R   K   Y   A   T   I   H   A   T   S   D   R   A   631

3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttatttttttcattggaattttttaacaa 3343
632  T   K   N   F   V   S   E   A   F   S   Y   F                                    643

3344 attcttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA 3405
644               D   M   V   P   F   E   K   V   V   Q   L   L   S   M   K   T   659

3406 TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT 3465
660  S   D   T   L   F   V   D   F   V   D   Y   W   T   K   S   S   S   E   I   F   679

3466 AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgttgaattgtaataaca 3532
680  K   M   L   K   E   H   L   S   G   H   I   V   K                               692
```

FIGURE 46 (cont.)

3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA 3593
693   I   G   N   S   Q   Y   L   Q   K   V   G   I   P   Q   G   S   708

3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG 3653
709 I   L   S   S   F   L   C   H   F   Y   M   E   D   L   I   D   E   Y   L   S   728

3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA 3713
729 F   T   K   K   K   G   S   V   L   L   R   V   V   D   D   F   L   F   I   T   748

3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgctgtcattcc 3777
749 V   N   K   K   D   A   K   K   F   L   N   L   S   L   R   G   764

3778 taagttctaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA 3840
765   F   E   K   H   N   F   S   T   S   L   E   K   T   V   778

3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA 3900
779 I   N   F   E   N   S   N   G   I   I   N   N   T   F   F   N   E   S   K   K   798

3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 3960
799 R   M   P   F   F   G   F   S   V   N   M   R   S   L   D   T   L   L   A   C   818

3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG 4020
819 P   K   I   D   E   A   L   F   N   S   T   S   V   E   L   T   K   H   M   G   838

4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataatcag A TCG 4089
839 K   S   F   F   Y   K   I   L   R   S   848

4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 4149
849 S   L   A   S   F   A   Q   V   F   I   D   I   T   H   N   S   K   F   N   S   868

4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 4209
869 C   C   N   I   Y   R   L   G   Y   S   M   C   M   R   A   Q   A   Y   L   K   888

4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtacttattttaactaga 4274
889 R   M   K   D   I   F   I   P   Q   R   M   F   I   T   D   903

4275 aaagtcattaattaaccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339
904   L   L   N   V   I   G   R   K   I   W   K   K   L   A   917

4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401
918 E   I   L   G   Y   T   S   R   R   F   L   S   S   A   E   V   K   W   935

4402 ggtctcgagacttcagcaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 4468
936   L   F   C   L   G   M   R   D   G   L   K   946

4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 4528
947 P   S   F   K   Y   H   P   C   F   E   Q   L   I   Y   Q   F   Q   S   L   T   966

4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA 4588
967 D   L   I   K   P   L   R   P   V   L   R   Q   V   L   F   L   H   R   R   I   986

4589 GCT GAT TAA tgtcattttcaatttattatatacatcctttattactggtgtcttaaacaatattattactaagtata 4665
987 A   D   *   989

FIGURE 46 (cont.)

```
4666  gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagttttgattgacttgtct  4745
4746  ttatccttatactttttaagaaagattgacagtggttgctgactactgcccacatgcccattaaacgggagtggttaaaca  4825
4826  ttaaaagtaatacatgaggctaatctcctttcatttagaataaggaaagtggttttctataatgaataatgcccgcacta  4905

4906  atgcaaaaagacgaagattatcttctaaacaaggggggattaagcatatccgaaggaaaagagagtaatatacccagtgtt  4985
4986  gttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattttggtgaccgaatttttggtaaaagc  5065
5066  cccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaatactaatagctcattta  5145
5146  atgtcttatataaggttttgttttttcctgacttcaatttttgcatgggtgaaaagaaatagtgttaagccattattggat  5225
5226  tccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc  5305
5306  tcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaattttttgc  5385
5386  aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatccttgatgtcaata  5465
5466  acttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaaggtacc  5544
```

FIGURE 47

```
                                  1
                                  met ser val tyr val val glu leu leu
GCCAAGTTCCTGCACTGGCTG             ATG AGT GTG TAC GTC GTC GAG CTG CTC


 10                                                       20
arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG


                        30
leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT


 40                                              50
gly ile arg gln his leu lys arg val gln leu arg glu leu ser
GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG


                        60
glu ala glu val arg gln his arg glu ala arg pro ala leu leu
GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG


 70                                              80
thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG


                        90
ile val asn met asp tyr val val gly ala arg thr phe arg arg
ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA


100                                             110
glu lys     ala glu arg leu thr ser arg val lys ala leu phe
GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC


                        120
ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC


130                                             140
ala ser val leu gly leu asp asp ile his arg ala trp arg thr
GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC


                        150
phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC


160                                             170
phe val lys val asp val thr gly ala tyr asp thr ile pro gln
TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG


                        180
asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC
```

FIGURE 47 (cont.)

```
190                                                 200
thr tyr cys val arg arg tyr ala val val gln lys ala ala met
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG


                          210
gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys
GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC


220                                                 230
gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser
CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC


                          240
leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG


250                                                 260
arg asp gly leu leu leu arg leu val asp asp phe leu leu val
CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG


                          270
thr pro his leu thr his ala lys thr phe leu arg thr leu val
ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC


280                                                 290
arg gly val pro glu tyr gly cys val val asn leu arg lys thr
CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA


                          300
val val asn phe pro val glu asp glu ala leu gly gly thr ala
GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT


310                                                 320
phe val gln met pro ala his gly leu phe pro trp cys gly leu
TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG


                          330
leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser
CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC


340                                                 350
tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly
TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC


                          360
phe lys ala gly arg asn met arg arg lys leu phe gly val leu
TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG


370                                                 380
arg leu lys cys his ser leu phe leu asp leu gln val asn ser
CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC
```

FIGURE 47 (cont.)

```
                    390
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400                                             410
ala tyr arg phe his ala cys val leu gln leu pro phe his gln
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

                    420
gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430                                             440
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

                    450
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460                                             470
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

                    480
thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490                                             500
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

                    510
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520                                             530
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

                    540
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550                                             560
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564
OP
TGA GTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC

CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC
```

FIGURE 47 (cont.)

AGGCTGGCGTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT

CCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCTTCGCCCTGCCTTCC

TTTGCCTTCCACCCCCACCATTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG

AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG

GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT

TTTCAGTTTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 48

Motif -1
Ep p123   ...LVVSLIRCFFYVTEQQKSYSKT...
Sp Tez1   ...FIIPILQSFFYITESSDLRNRT...
Sc Est2   ...LIPKIIQTFFYCTEISSTVTIV...
Hs TCP1   ...YVVELLRSFFYVTETTFQKNRL...
consensus   FFY TE

                     K
Motif 0   p hhh K   hR h   R
Ep p123   ...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...
Sp Tez1   ...QKTTLPPAVIRLLPKKN--TFRLITNLRKRFL...
Sc Est2   ...TLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD...
Hs TCP1   ...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...
consensus   R PK   R I

                 AF
Motif A   h hDh GY h
Ep p123   ...PKLFFATMDIEKCYDSVNREKLSTFLK...
Sp Tez1   ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
Sc Est2   ...PELYFMKFDVKSCYDSIPRMECMRILK...
Hs TCP1   ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
consensus   F D YD

Motif B   hPQG pS hh
Ep p123   ...NGKFYKQTKGIPQGLCVSSILSSFYYA...
Sp Tez1   ...GNSQYLQKVGIPQGSILSSFLCHFYME...
Sc Est2   ...EDKCYIREDGLFQGSSLSAPIVDLVYD...
Hs TCP1   ...RATSYVQCQGIPQGSILSTLLCSLCYG...
consensus   G QG S

                 Y
Motif C   h F DDhhh
Ep p123   ...PNVNLLMRLTDDYLLITTQENN...

Sp Tez1   ...KKGSVLLRVVDDFLFITVNKKD...
Sc Est2   ...SQDTLILKLADDFLIISTDQQQ...
Hs TCP1   ...RRDGLLLRLVDDFLLVTPHLTH...
consensus   DD L

Motif D   Gh h cK
Ep p123   ...NVSRENGFKFNMKKL...
Sp Tez1   ...LNLSLRGFEKHNFST...
Sc Est2   ...KKLAMGGFQKYNAKA...
Hs TCP1   ...LRTLVRGVPEYGCVV...
consensus   G

FIGURE 49

BSPH1 6978
APAL1 6810
DRA3 225
XHO1 674
ECOR5 701
ECOR1 707
NOT1 713
MSC1 852

BSPH1 5970

F1ori
Amp Pro
Ampsig
AmpR
T7pro

APAL1 5564

ORI

SMA1 1430
SMA1 1550

pGRN121
7056 bp

ORF

SMA1 2053

FFYVTE
PKP
AYD
QG
DD

T3pro

SAC2 4844
NOT1 4834
BAMH1 4816
SMA1 4810
ECOR1 4798
SAC2 4779

MSC1 2397

XHO1 2740
ECOR5 2828

MSC1 4174
SMA1 4095
APAL1 3766
SAC2 3658

DRA3 3221
BAMH1 3264
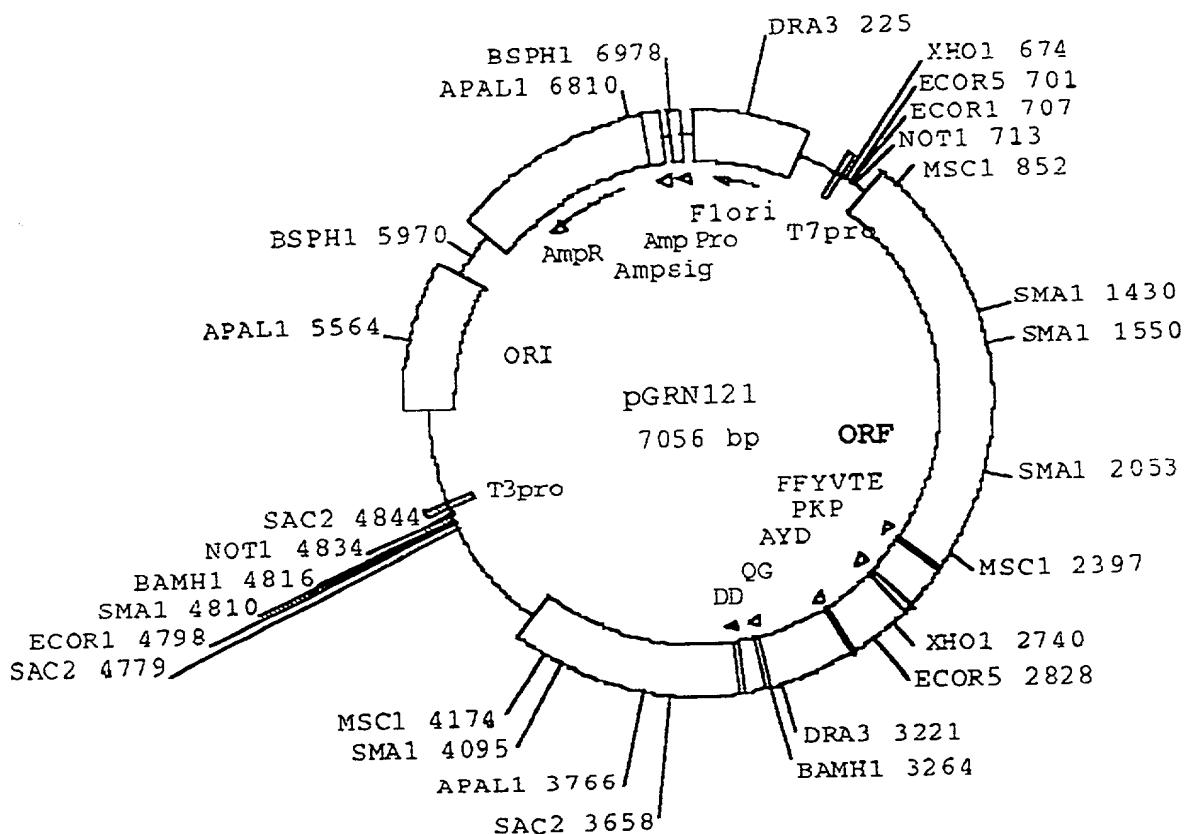
FIGURE 50

```
   1 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC
  51 CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC
 101 AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG
 151 GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCCGCG
 201 CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN ANGGCNGCCC
 251 CCCGCCGCCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC
 301 CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT
 351 TCGGCTTCGC GCTGCTGGAC GGGGCCCGCG GGGGCCCCCC CGAGGCCTTC
 401 ACCACCAGCG TGCGCAGCTA CCTGCCCAAC ACGGTGACCG ACGCACTGCG
 451 GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG CCGCGTGGGC GACGACGTGC
 501 TGGTTCACCT GCTGGCACGC TGCGCGNTNT TTGTGCTGGT GGNTCCCAGC
 551 TGCGCCTACC ANGTGTGCGG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC
 601 TCAGGCCCGG CCCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC
 651 CAACGGGCCT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG
 701 CCAGCCCCGG GTGCGAGGAG CGCGGGGGGC AGTGCCAGCC GAAGTCTGCC
 751 GTTGCCCAAG AGGCCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC
 801 CCGTTGGGCA GGGGTCCTGG GCCCACCCGG GCAGGACGCC TGGACCGAGT
 851 GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC
 901 CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG
 951 GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT
1001 GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCCTCTAC
1051 TCCTCAGGCG ACAAGNACAC TGCGNCCCTC CTTCCTACTC AATATATCTG
1101 AGGCCCAGCC TGACTGGCGT TCGGGAGGTT CGTGGAGACA NTCTTTCTGG
1151 TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCC GCCTGCCCCA
1201 GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGGAACCACG
1251 CGCAGTGCCC CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT
1301 GCGGTCACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC
1351 TGTGGCGGCC CCCGAGGAGG AGGAACACAG ACCCCGTCG CCTGGTGCAG
1401 CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGCGGGC
1451 CTGCCTGCGC CGGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG
1501 AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT
1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGCGGGACTG
1601 CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC
1651 ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT
1701 GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC
1751 GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT
1801 TGCAAAGCAT TGGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG
1851 CTGTCGGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT
1901 GACGTCCAGA CTCCGCTTCA TCCCCAAGCC TGACGGGCTG CGGCCGATTG
1951 TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCCGCAG AGAAAAGAGG
2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTCAGCG TGCTCAACTA
2051 CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG
2101 ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCCAG
2151 GACCCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA
2201 CGACACCATC CCCCAGGACA GGCTCACGGA GGTCATCGCC AGCATCATCA
2251 AACCCCAGAA CACGTACTGC GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC
```

FIGURE 50 (cont.)

2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC
2351 AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA
2401 GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG
2451 GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC
2501 CGTGCGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG
2551 GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG
2601 AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TGCGTTTGGT
2651 GGATGATTTC TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC
2701 TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG
2751 CGGAAGACAG TGGTGAACTT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC
2801 GGCTTTTGTT CAGATGCCGG CCCACGGCCT ATTCCCCTGG TGCGGCCTGC
2851 TGCTGGATAC CCGGACCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC
2901 CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT TCAAGGCTGG
2951 GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTCACA
3001 GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC
3051 ATCTACAAGA TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT
3101 GCAGCTCCCA TTTCATCAGC AAGTTTGGAA GAACCCCACA TTTTTCCTGC
3151 GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG
3201 AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC CTCTGCCCTC
3251 CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC
3301 GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCCAG
3351 ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC
3401 CGCAGCCAAC CCGGCACTGC CCTCAGACTT CAAGACCATC CTGGACTGAT
3451 GGCCACCCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC
3501 GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCCACAC CCAGGCCCGC
3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT
3601 CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA
3651 GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG
3701 CTCGGCTCCA CCCCAGGGCC AGCTTTTCCT CACCAGGAGC CCGGCTTCCA
3751 CTCCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC
3801 GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG GAGACCCTGA
3851 GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG
3901 TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT
3951 GGGGGGGAGGT GCTGTGGGAG TAAAATACTG AATATATGAG TTTTTCAGTT
4001 TTGAAAAAAA AAAAAAAAAA AAAAAAAA

FIGURE 51

```
     GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC
  1  ---------+---------+---------+---------+---------+---------+  60
     CGTCGCGACGCAGGACGACGCGTGCACCCTTCGGGACCGGGGCCGGTGGGGGCGCTACGG

a       A  A  L  R  P  A  A  H  V  G  S  P  C  F  G  H  P  R  D  A  -
b        Q  R  C  V  L  L  R  T  W  E  A  L  A  P  A  T  P  A  M  P  -
c          S  A  A  S  C  C  A  R  G  K  P  W  F  R  P  P  F  R  C  R  -

     CCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT
 61  ---------+---------+---------+---------+---------+---------+ 120
     CGCGCGAGGGGCGACGGCTCGGCACGCGAGGGACGACGCGTGGTGATGGCGCTCCACGA

a       A  R  S  P  L  F  S  R  A  L  P  A  A  Q  P  L  P  R  G  A  -
b        R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  -
c          A  L  P  A  A  E  P  C  A  P  C  C  A  A  T  T  A  R  C  C  -

     GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG
121  ---------+---------+---------+---------+---------+---------+ 180
     CGGCGACCGGTGCAAGCACGCCGCGGACCCCGGGGTCCCGACCGCCGACCACGTCGCGCC

a       A  A  G  H  V  R  A  A  P  G  A  P  G  L  A  A  G  A  A  R  -
b        P  L  A  T  F  V  R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  -
c          R  W  P  R  S  C  G  A  W  G  P  R  A  G  G  W  C  S  A  G  -

     GGACCCGGCGGCTTTCCGCGCGNTGGTGGCCCANTGCNTGGTGTGCGTGCCCTGGGANGN
181  ---------+---------+---------+---------+---------+---------+ 240
     CCTGGGCCGCCGAAAGGCGCGCNACCACCGGGGTNACGNACCACACGCACGGCACCCTNCN

a       G  P  G  G  F  P  R  ?  G  G  P  ?  ?  G  V  R  A  L  G  ?  -
b        D  P  A  A  F  R  A  ?  V  A  ?  C  ?  V  C  V  P  W  ?  ?  -
c          T  R  R  L  S  A  R  W  W  P  ?  A  W  C  A  C  L  G  ?  ?  -

     ANGGCNGCCCCCCGCCGCCCCCTCCTTCCGCCAGGTGTCCTGCTGAANGANCTGGTGGC
241  ---------+---------+------ -- --+---------+---------+---------+ 300
     TNCCGNCGGCGGGCGGCGGGGGAGGAAGGCGGTCCACAGGACGGACTTNCTNGACCACCG

a       ?  A  A  F  R  R  P  L  L  P  P  G  V  L  P  E  ?  ?  G  G  -
b        ?  ?  P  P  A  A  P  S  F  R  G  V  S  C  L  ?  ?  L  V  A  -
c          G  ?  P  P  P  P  P  P  S  A  R  C  P  A  ?  ?  ?  W  W  P  -

     CCGAGTGCTGCANANGCTGTGCGANCCCGGCGGCGAANAACGTGCTGGCCTTCGGCTTCGC
301  ---------+---------+---------+---------+--------  +  ------+ 360
     GGCTCACGACGTNTNCGACACGCTNGCGCCGCGCTNTTYCACGACCGGAAGCCGAAGCG

a       P  S  A  A  ?  A  V  R  ?  R  R  E  ?  R  A  G  L  R  L  R  -
b        R  V  L  ?  ?  L  C  ?  R  G  A  ?  N  V  L  A  F  G  F  A  -
c          E  C  C  ?  ?  C  A  ?  A  A  R  ?  T  C  W  P  S  A  S  R  -

     GCTGCTGGACGGGGCCCGCGGGGGGCCCCCCCCAGCGCCPTCACCACCAGCGTGCGCAGCTA
361  ---------+---------+---------+---------+---------+--------  + 420
     CGACGACCTGCCCCGGGCGCCCCCCGCGGCGGCTCCGGAAGTGGTGGTCGCACGCGTCGAT

a       A  A  G  R  G  P  R  G  P  P  R  G  L  H  H  Q  R  A  Q  L  -
b        L  L  D  G  A  R  G  G  F  P  E  A  F  T  T  S  V  R  S  Y  -
c          C  W  T  G  P  A  G  A  P  F  R  P  S  P  P  A  C  A  A  T  -
```

FIGURE 51 (cont.)

```
              CCTGCCCAACACGGTGACCGACGCACTGCGGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCG
          421 ---------+---------+---------+---------+  · ·····+········  + 480
              GGACGGGTTGTGCCACTGGCTGCGTGACGCCCCCTCGCCCGCACCCCCGACGACGACGC

           a    P  A  Q  H  G  D  R  R  T  A  G  E  P  G  V  G  A  A  A  A
           b    L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  -
           c    C  P  T  R  *  P  T  H  C  G  G  A  G  R  G  G  C  C  A  -

              CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTXCGCNTNTTCTCCTGCT
          481 ---------+---------+---------+---------+---------+---------+ 540
              GGCGCACCCGCTGCTGCACGACCAAGTGGACGACCGTGCGACGCGCNANAAACACGACTA

           a    P  R  G  R  R  R  A  G  S  P  A  G  T  L  R  ?  ?  C  A  G  -
           b    R  V  G  D  D  V  L  V  H  L  L  A  R  C  A  ?  T  V  L  V  -
           c    A  W  A  T  T  C  W  F  T  C  W  H  A  A  R  ?  L  C  W  W  .

              GGNTCCCACCTGCGGCCTACCANGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCNAC
          541 ---------+---------+---------+ ·········+·········+---------+ 600
              CCNAGGGTCGACGCCGGATGGTNCACACGCCCGGCGGCGACATGGTCGAGCCGCGACGNTG

           a    G  S  Q  L  R  L  P  ?  V  R  A  A  A  V  P  A  R  R  C  ?  -
           b    ?  P  S  C  A  Y  ?  V  C  G  P  P  L  Y  Q  L  G  A  A  T  -
           c    ?  F  A  A  P  T  ?  C  A  G  R  R  C  T  S  A  L  ?  L  -

              TCAGGCCCGGCCCCCGCCACACCCTANTCGACCCCGAANCCGTCTCGGCATCCAACCCGCCT
          601 ·   ------+---------+---------+---------+---------+---------+ 660
              ACTCCGGGCCGGGGGCGGTGTGGGGATNACCTGGGCTTNCGCAGACCCTAGGTTGCCCGGA

           a    S  C  P  A  P  A  T  R  ?  W  T  R  ?  R  L  G  S  N  G  P  -
           b    Q  A  R  P  P  P  H  A  ?  G  P  E  ?  V  W  D  P  T  G  L  -
           c    R  P  G  P  R  H  T  L  ?  D  P  ?  A  S  G  I  Q  R  A  W

              GGAACCATAGCGTCAGCGAGGCCCCGCGTCCCCCTCGCCTCCCACCCCCGGGTCCGACCAG
          661 ---------+---------+---------+---------+---------+---------+ 720
              CCTTGGTATCGCAGTCGCTCCGGGGCGCAGGGGGAGCGGAGCGGTCGGGGCCCACGGCTCCTC

           a    G  T  I  A  S  C  R  P  C  S  P  W  A  A  S  P  G  C  E  E  -
           b    E  P  *  R  Q  G  G  R  C  P  P  G  L  P  A  P  G  A  R  R  -
           c    N  H  S  V  R  E  A  G  V  P  L  G  C  Q  P  R  V  R  G  G  -

              GCGCCGGCCCCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGACGCCCAGGCGTCGCGCTGC
          721 ---------+---------+---------+---------+---------+---------+ 780
              CGCGGCCGGGGTCACGGTCGGCTTCAGACGGCAACGGGTTCTGCGGGTCCGCACCGCGACG

           a    A  R  G  Q  C  Q  P  K  S  A  V  A  Q  E  A  Q  A  W  R  C  -
           b    R  G  G  S  A  S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  -
           c    A  G  A  V  P  A  E  V  C  R  C  P  R  G  P  G  V  A  L  ?  -

              CCCTNAGCCCCACCCGACCCCCGTTCGCCAGCGGGTCCTCGGCCCACCCGGGCAGGACGCC
          781 ---------+---------+---------+---------+---------+---------+ 840
              GGGACTCGGGGTGGGCTGCGGGCAACCGGTCCCCAGGACCCGGGTGGGCCCGTCCTGCGG

           a    P  *  A  C  A  D  A  R  W  A  C  V  L  G  P  P  G  Q  D  ?  -
           b    P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  P  -
           c    L  S  R  S  G  R  P  L  G  R  G  P  G  P  T  R  A  G  R  L  -
```

FIGURE 51 (cont.)

```
     TGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCCGCCCAAGAAGCCAC
841  --------- + --------- + --------- + --------- + --------- + --------- +  900
     ACCTGGCTCACTGGCACCAAAGACACACCACAGTGGACGGTCTGGGCGGCCTTCTTCGGTG

a    W  T  E  *  P  W  F  L  C  G  V  T  C  Q  T  R  R  R  S  H  -
b    G  P  S  D  R  G  F  C  V  V  S  P  A  R  P  A  E  E  A  T
c    D  R  V  T  V  V  S  V  W  C  H  L  P  D  P  P  K  K  P  -

     CTCTTTGGAGGGTCCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGGCCAGCA
901  --------- + --------- + -------- -+ --------- + --------- + --------- +  960
     GAGAAACCTCCCACGCGAGAGACCGTGCGCGGTGAGGGTGGGTAGGCACCCGGCCGGTCGT

a    L  F  G  G  C  A  L  W  H  A  P  L  P  P  T  R  G  F  F  A
b    S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  -
c    L  W  R  V  R  S  L  A  R  A  T  P  T  H  P  W  A  A  S  T  -

     CCACGCGGGCCCCCATCCACATCGCGGCCACCACGTCCTGGGACACGCCTTGTCCCCCG
961  --------- + --- --+ --------- + --------- + --------- + --------- +  1020
     GGTGCGCCCGGGGGGTAGGTGTAGCGCCGGTGGTGCAGGACCCTGTGCGGAACAGGGGGC

a    P  R  G  P  P  I  H  I  A  A  T  T  S  W  D  T  P  C  P  P
b    H  A  G  P  P  S  T  S  R  P  P  R  P  G  T  R  L  V  P  R
c    T  R  A  F  H  H  P  H  R  G  H  H  V  L  G  H  A  L  S  P  G  -

     GTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGNACACTGCGNCCCTC
1021 --------- + --------- + --------- + --------- + --------- + --------- +  1080
     CACATGCGGCTCTGGTTCGTGAAGGAGATGAGGAGTCCGCTGTTCNTGTGACGCNGGGAG

a    V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  ?  T  A  ?  L  -
b    C  T  P  R  P  S  T  S  S  T  P  Q  A  T  ?  T  L  R  P  ?  -
c    V  R  R  D  Q  A  L  P  L  L  L  R  R  Q  ?  H  C  ?  P  P  -

     CTTCCTACTCAATATATCTGAGGCCCAGCCTGACTGGCGTTCGGGAGGTTCGTGGAGACA
1081 --------- + --------- + --------- + --------- + --------- + --------- +  1140
     GAAGGATGAGTTATATAGACTCCGGGTCGGACTGACCGCAAGCCCTCCAAGCACCTCTGT

a    L  P  T  Q  Y  I  *  G  P  A  *  L  A  F  G  R  F  V  E  T
b    F  L  L  N  I  S  E  A  Q  P  D  W  R  S  G  G  S  W  R  ?  -
c    S  Y  S  I  Y  L  R  P  S  L  T  G  V  R  E  V  R  G  D  ?  -

     NTCTTTCTGGTTCCAGGCCTTGGATGCCAGGATTCCCCGCAGGTTGCCCGCCTGCCCCA
1141 --------- + --------- + --------- + --------- + --------- + --------- +  1200
     NAGAAAGACCAAGGTCCGGAACCTACGGTCCTAAGGGGCGTCCAACGGGCGGACGGGGT

a    ?  F  L  V  P  G  L  G  C  Q  D  S  P  Q  V  A  P  P  A  P  -
b    S  F  W  F  Q  A  L  D  A  R  I  P  R  R  L  P  R  L  P  Q  -
c    L  S  G  S  R  P  W  M  P  G  F  P  A  G  C  P  A  C  P  S  -

     GCGNTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCC
1201 --------- + --------- + --------- + --------- + --------- + --------- +  1260
     CGCNATGACCGTTTACGCCGGGGACAAAGACCTCGACGAACCCTTGGTGCGCGTCACGGG

a    A  ?  L  A  N  A  A  P  V  S  G  A  A  W  E  P  R  A  V  P  -
b    R  Y  W  Q  M  R  F  L  F  L  E  L  L  G  N  H  A  Q  C  ?  -
c    ?  T  G  K  C  G  P  C  F  W  S  C  L  G  T  T  R  S  A  ?  -
```

FIGURE 51 (cont.)

```
        CTACGRGGTGTTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCGGG
1261    .  ----+---------+---------+---------+---------+---------+  1320
        GATGCCCACAAGGAGTTCTGCGTGACGGGCGACGCTCGACGCCAGTGGGGTCGTCGGCC

a    L  R  G  V  P  Q  D  A  L  F  A  A  S  C  G  H  F  S  S  R  -
b    Y  G  V  F  L  K  T  H  C  P  L  R  A  A  V  T  P  A  A  G  -
c    T  G  C  S  S  R  R  T  A  R  C  E  L  R  S  P  Q  Q  F  V  -


        TGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGAACACAG
1321    ---------+---------+---------+---------+---------+---------+  1380
        ACAGACACGGGCCCTCTTCGGGGTCCCGAGACACCGCCGGGGGCTCCTCCTCCTTGTGTC


a    C  L  C  P  G  E  A  P  G  L  C  G  G  P  R  G  G  G  T  Q  -
b    V  C  A  R  E  K  P  Q  G  S  V  A  A  P  E  E  E  E  H  R  -
c    S  V  P  G  R  S  P  R  A  L  W  R  P  P  R  R  R  N  T  D  -


        ACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCT
1381    ---------+---------+---------+---------+---------+---------+  1440
        TGGGGGCAGCGGACCACGTCGACGAGGCGGTCGTGTCGTCGGGGACCGTCCACATGCCGA


a    T  P  V  A  W  C  S  C  S  A  S  T  A  A  P  G  R  C  T  A  -
b    P  P  S  P  G  A  A  A  P  P  A  Q  Q  P  L  A  G  V  R  L  -
c    P  R  R  L  V  Q  L  L  R  Q  H  S  S  P  W  Q  V  Y  G  F  -


        TCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGCCACAACG
1441    ---------+---------+---------+---------+---------+---------+  1500
        AGCACGCCCGGACGGACGCGGCCGACCACGGGGGTCCGGAGACCCCGAGGTCCGTGTTGC


a    S  C  G  P  A  C  A  G  W  C  P  Q  A  S  G  A  F  G  T  T  -
b    R  A  G  L  P  A  P  A  G  A  P  R  P  L  G  L  Q  A  Q  R  -
c    V  R  A  C  L  R  R  L  V  P  P  G  L  W  G  S  R  H  N  E  -


        AACGCCGCGTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCCAAGCTCT
1501    ---------+---------+---------+---------+-----  --+---------+  1560
        TTGCGGCGCAAGGAGTCCTTGTGGTTCTTCAACTAGAGGGACCCCTTCGTACGGGTTCGAGA


a    N  A  A  S  S  G  T  P  R  S  S  S  P  W  G  S  M  P  S  S  -
b    T  P  L  P  Q  E  H  Q  E  V  H  L  P  G  E  A  C  Q  A  L  -
c    R  R  F  L  R  N  T  K  K  F  I  S  L  G  K  H  A  R  L  S  -


        CGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCCCAGGAGCC
1561    ---------+---------+------- --+---------+---------+---------+  1620
        GCGACGTCCTCGACTGCACCTTCTACTCGCACGCCCTGACGCGAACCGACGGGTCCTCGG


a    R  C  R  S  *  R  G  R  *  A  C  G  T  A  L  G  C  A  G  A  -
b    A  A  G  A  D  V  E  D  E  R  A  G  L  R  L  A  A  Q  E  P  -
c    L  Q  E  L  T  W  K  M  S  V  R  D  C  A  W  L  R  R  S  P  -


        CAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTCCCTGAGGAGATCCTGGCCAAGT
1621    ---------+---------+---------+---------+---------+. . ------+  1680
        GTCCCCAACCGACACAAGGCCGGCGTCTCGTGGCAGACGCACTCCTCTAGGACCGGTTCA


a    Q  G  L  A  V  F  R  P  Q  S  T  V  S  L  R  R  S  W  P  S  -
b    R  G  W  L  C  S  G  R  R  A  P  S  A  *  G  D  P  G  Q  V  -
c    G  V  G  C  V  P  A  A  E  H  R  L  R  E  E  I  L  A  K  F
```

FIGURE 51 (cont.)

```
      TCCTGCACTGCCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCA
1681  ------------+---------+---------+---------+---------+--- -----+ 1740
      AGGACGTGACCGACTACTCACACATGCAGCAGCTCGACGAGTCCAGAAACAAAATACAGT

a     S  C  T  G  *  *  V  C  T  S  S  S  C  S  C  L  S  F  M  S  -
b     P  A  L  A  D  E  C  V  R  R  R  A  A  Q  V  F  L  L  C  H  -
c     L  H  W  L  M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T  -

      CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGT
1741  --------+---------+--- ---+  -  ---+   ---+   -- +  ------+ 1800
      GCCTCTGGTGCAAACTTTTCTTCTCCGAGAAAAAGATCGCCTTCTCACAGACCTCCTTCA

a     R  R  P  F  K  R  T  G  S  F  S  T  G  R  V  S  G  A  S  -
b     G  D  H  V  S  K  E  Q  A  L  F  L  P  E  E  C  L  E  Q  V  -
c     E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L  -

      TGCAAACCATGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAG
1801  ---------+---------+---------+---------+---------+---------+ 1860
      ACGTTTGGTAACCTTAGTCTGTCGTGAACTTCTCCCACGTCGACGCCCTCGACAGCCTTC

a     C  K  P  W  N  Q  T  A  L  E  E  G  A  A  A  G  A  V  G  S  -
b     A  K  H  W  N  Q  T  A  L  E  E  G  A  A  A  G  A  V  G  S  -
c     Q  S  T  G  T  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A  -

      CAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCA
1861  ---------+---------+---------+---------+---------+---------+ 1920
      GTCTCCAGTCCGTCGTAGCCCTTCGGTCCGGGCGGGACGACTGCAGGTCTGAGGCGAAGT

a     Q  R  S  G  S  I  G  K  P  G  P  P  C  *  R  F  D  S  A  S  -
b     R  G  Q  A  A  S  G  S  Q  A  R  P  A  D  V  Q  T  P  L  H  -
c     E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I  -

      TCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAA
1921  - ---+---------+---------+----- --+    --+---------+ 1980
      AGGGGTTCGGACTGCCCGACGCCGGCTAACACTTGTACCTGATGCAGCACCCTCGGTCTT

a     S  P  S  L  T  G  C  G  R  L  *  T  W  T  T  S  W  E  P  R  -
b     P  Q  A  *  R  A  A  A  D  C  E  H  G  L  R  R  G  S  Q  N  -
c     P  K  P  D  G  L  R  P  I  V  N  M  D  Y  V  V  G  A  R  T  -

      CGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCG
1981  ---------+---------+---------+---------+--------- +  ------+ 2040
      GCAAGGCGTCTCTTTTCTCCCGGCTCGCAGAGTGGAGCTCCCACTTCCGTGACAAGTCGC

a     R  S  A  E  K  R  G  P  S  V  S  P  R  G  *  R  H  C  S  A  -
b     V  P  Q  R  K  E  G  R  A  S  H  L  E  G  E  G  T  V  Q  R  -
c     F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V  -

      TGCTCAACTACGACCCGGCCGGCGCCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGG
2041  ---------+---------+---------+---------+---------+ ---------+ 2100
      ACGAGTTGATGCTGCCGGCGCCGCCGCGGGCCCCCAGCACCCGCGGAGACACGACCCGGACC

a     C  S  T  T  S  G  E  G  A  P  A  S  W  A  P  L  C  W  A  W  -
b     A  Q  L  R  A  G  A  A  P  R  P  P  G  R  L  C  A  G  P  G  -
c     L  N  Y  E  R  A  R  R  P  G  L  L  G  A  S  V  L  G  L  D  -
```

FIGURE 51 (cont.)

```
       ACGATATCCACAGGGCCTGGCGCACCTTGGTGCTGCGTGTGGGGCCCAGGACCCGCCCC
2101   ---------+---------+---------+------ --  +  ---------+---------+ 2160
       TGCTATAGGTGTCCCGGACCGCGTGGAAGCACGACGCACACGCCCGGGTCCTGGCCCCCG
```

```
a      T  I  S  T  C  P  G  A  P  S  C  C  V  C  G  F  R  T  R  R   -
b      R  Y  F  Q  G  L  A  H  L  R  A  A  C  A  C  P  G  P  A  A   -
c      D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P   -
```

```
       CTCAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGGGTACGACACCATCCCCCAGGACA
2161   ---------+---------+---------+---------+---------+---------+ 2220
       GACTCGACATGAAACAGTTCCACCTACACTGCCCGCCCATGCTGTGGTAGGGGGTCCTGT
```

```
a      L  S  C  T  L  S  R  W  M  *  R  A  P  T  T  P  S  P  R  T   -
b      *  A  V  L  C  Q  G  G  C  D  G  R  V  R  H  H  P  P  G  Q   -
c      E  L  Y  F  V  K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  R   -
```

```
       GCCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGT
2221   ---------+---------+---------+---------+---------+---------+ 2280
       CGGAGTGCCTCCAGTAGCGGTCGTAGTAGTTTGGGGTCTTGTGCATGACGCACGCAGCCA
```

```
a      G  S  R  R  S  S  P  A  S  S  N  P  R  T  R  T  A  C  V  G   -
b      A  H  G  G  H  R  Q  H  H  Q  T  P  E  H  V  L  R  A  S  V   -
c      L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y   -
```

```
       ATGCCGTGGTCCAGAACGCCCCCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCT
2281   ---------+---------+---------+---------+---------+---------+ 2340
       TACGGCACCAGGTCTTGCGGCGGGTACCCGTGCAGGCGTTCCGGAAGTTCTCGGTGCAGA
```

```
a      M  P  W  S  R  R  P  P  M  G  T  S  A  R  P  S  R  A  T  S   -
b      C  R  G  P  E  G  R  P  W  A  R  P  Q  G  L  Q  E  P  R  L   -
c      A  V  V  Q  K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S   -
```

```
       CTACCTTGACAGACCTCCAGCCGTACATCCCACAGTTCCTGGCTCACCTGCAGCANAACA
2341   ---------+---------+---------+---------+---------+---------+ 2400
       GATGGAACTGTCTGGAGGTCGGCATGTACGCTGTCAAGCACCGAGTGGACGTCTNTTGT
```

```
a      L  P  *  Q  T  S  S  R  T  C  D  S  S  W  L  T  C  R  ?  T   -
b      Y  L  D  R  P  P  A  V  H  A  T  V  R  G  S  P  A  G  ?  Q   -
c      T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  ?  N  S   -
```

```
       GCCCGCTCACCGATCCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTG
2401   ---------+---------+---------+---------+---------+---------+ 2460
       CGGGCGACTCCCTACGGCAGCAGTAGCTCGTCTCGAGGAGGGACTTACTCCGGTCGTCAC
```

```
a      A  R  *  G  M  P  S  S  S  S  R  A  P  P  *  M  R  P  A  V   -
b      P  A  E  G  C  R  R  H  R  A  E  L  L  P  E  *  G  Q  Q  W   -
c      P  L  R  D  A  V  V  I  E  Q  S  S  S  L  N  E  A  S  S  G   -
```

```
       GCCTCTTCGACGTCTTCCTACGCTTCATCTGCCACCACGCCGTCCGCATCAGGGGCAAGT
2461   ---------+---------+---------+---------+---------+---------+ 2520
       CGGAGAAGCTGCAGAAGGATGCGAAGTACACGGTGGTGCGGCACGGCGTAGTCCCCGTTCA
```

```
a      A  S  S  T  S  S  Y  A  S  C  A  T  T  P  C  A  S  G  A  S   -
b      P  L  R  R  L  P  T  L  H  V  P  P  R  R  A  H  Q  G  Q  V   -
c      L  F  D  V  F  L  R  F  M  C  H  H  A  V  R  I  R  G  K  S   -
```

FIGURE 51 (cont.)

```
      CCTACCTCCAGTCCCAGCGGGATCCCCCACGGGCTCCATCCTCTCTCCACCCTGCTCTGCAGCC
2521  ---------+---------+---------+---------+---------+---------+  2580
      GGATGGAGGTCACGGTCCCCTAGGGGCGTCCCGAGGGTAGGAGAGGGTGCGACGAGACGTCGG

a         P  T  S  S  A  R  G  S  R  R  A  P  S  S  P  P  C  S  A  A  -
b         L  P  P  V  P  G  D  P  A  G  L  H  P  L  H  A  A  L  Q  P  -
c         Y  V  Q  C  Q  G  I  P  Q  G  S  I  L  S  T  L  L  C  S  L  -

      TGTGCTACGGCGGACATGGAGAACAAGCTGTTTGCGGGGGATTGGGCGGGACGGGCTGCTCC
2581  ---------+---------+--- ---  +  -      +         .+---------+  2640
      ACACGATGCCGCTGTACCTCTTGTTCGACAAACGCCCCTAAGCCGCCCTGCCCGACGAGG

a         C  A  T  A  T  W  R  T  S  C  L  R  C  F  G  G  T  C  C  S  -
b         V  L  R  R  H  G  E  Q  A  V  C  G  D  S  A  G  R  A  A  P  -
c         C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R  D  G  L  L  L  -

      TGCGTTTGGTGGATGATTTCTTGTTCGTCACACCTCACCTCACCCACGCGAAAACCTTCC
2641  ---------+---------+---------+---------+---------+---------+  2700
      ACGCAAACCACCTACTAAAGAACAACCACTGTGGAGTGGAGTGGGTGCGCTTTTGGAAGG

a         C  V  W  W  M  I  S  C  W  *  H  L  T  S  P  T  R  K  P  S  -
b         A  F  G  G  *  F  L  V  G  D  T  S  P  H  P  R  E  N  L  P  -
c         R  L  V  D  D  F  L  L  V  T  P  H  L  T  H  A  K  T  F  L  -

      TCAGGACCCTGGTCCCACGTCTCCCTCACTATGGCTGCGTGGTGAACTTGCGGAAGACAG
2701  ---------+---------+---------+---------+---------+---------+  2760
      AGTCCTGGGACCAGGCTCCACAGGGACTGATACCGACGCACCACTTGAACGCCTTCTGTC

a         S  G  P  W  S  E  V  S  L  S  M  A  A  W  *  T  C  G  R  Q  -
b         Q  D  P  G  P  R  C  P  *  V  W  L  R  G  E  L  A  E  D  S  -
c         P  T  L  V  R  G  V  P  F  Y  G  C  V  V  N  L  R  K  T  V

      TGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGG
2761  ---------+---------+---------+---------+---------+---------+  2820
      ACCACTTGAAGGGACATCTTCTGCTCCGGGACCCACCGTGCCGAAAACAAGTCTACGGCC

a         W  *  T  S  L  *  K  T  R  P  W  V  A  R  L  L  F  R  C  R  -
b         G  E  L  P  C  R  R  R  G  P  G  W  H  G  F  C  S  D  A  G  -
c         V  N  F  P  V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A  -

      CCCACGGCCTATTCCCCTGGTCCGCCCTGCTGCTGCATACCCGGACCCTCGAGGTCCACA
2821  ---------+---------+---------+---------+---------+---------+  2880
      GGGTGCCGGATAAGGGGACCAGGCGGGACGACGACGTATGGGCCTGGGACCTCCAGGTGT

a         P  T  A  Y  S  P  G  A  A  C  C  W  I  P  G  P  W  R  C  R  -
b         P  R  P  I  P  L  V  R  P  A  A  G  Y  P  D  P  G  G  A  E  -
c         H  G  L  F  P  W  C  G  L  L  L  C  T  R  T  L  E  V  Q  S  -

      GCGACTACTCCAGCTATCCCCCCACCTCCATCAGAGCCACTCTCACCTTCAACCGCGGCT
2881  ---------+---------+---------+---------+---------+---------+  2940
      CGCTGATGAGGTCGATACGGGCCTGGAGGTAGTCTCGGTCAGAGTGGAAGTTGGCGCCGA

a         A  T  T  P  A  M  P  G  P  P  S  E  P  V  S  P  S  T  A  A  -
b         R  L  L  Q  L  C  P  D  L  H  Q  S  Q  S  H  L  Q  P  R  L  -
c         D  Y  S  S  Y  A  R  T  S  I  R  A  S  L  T  F  N  R  G  F  -
```

FIGURE 51 (cont.)

```
         TCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACA
2941     ---------+---------+---------+---------+---------+---------  3000
         AGTTCCGACCCTCCTTGTACGCAGCCGTTTGAGAAACCCCAGAACGCCGACTTCACAGTGT
```

```
a        S  F  L  G  G  T  C  V  A  N  S  L  G  S  C  G  *  S  V  T
b        Q  G  W  E  E  H  A  S  Q  T  L  W  G  L  A  A  E  V  S  Q
c        K  A  G  R  N  M  R  R  K  L  F  G  V  L  R  L  K  C  H  S  -
```

```
         GCCTGTTTCTCCATTTCCACCTCAACAGCCTCCACACGCTGTCCACCAACATCTACAAGA
3001     ---------+---------+---------+---------+---------+---------  3060
         CGGACAAAGAGGTAAAGGTGGAGTTGTCGGAGGTGTCTGCCACACGTGGTTGTAGATGTTCT
```

```
a        A  C  F  W  I  C  R  *  T  A  S  K  R  C  A  F  T  S  T  K  -
b        P  V  S  G  F  A  G  E  Q  F  P  D  G  V  H  Q  H  L  Q  D  -
c        L  F  L  D  L  Q  V  N  S  L  Q  T  V  C  T  N  I  Y  K  T  -
```

```
         TCCTCCTGCTCCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGC
3061     ---------+---------+---------+---------+---------+---------  3120
         AGGAGGACGACGTCCGCATGTCCAAAGTGCGTACACACGACGTCGAGGGTAAAGTAGTCG
```

```
a        S  S  C  C  R  R  T  G  F  T  H  V  C  C  S  S  H  F  I  S  -
b        P  P  A  A  G  V  Q  V  S  R  M  C  A  A  A  P  I  S  S  A  -
c        L  L  L  Q  A  Y  R  F  H  A  C  V  L  Q  L  P  F  H  Q  Q  -
```

```
         AAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCT
3121     ---------+---------+---------+---------+---------+---------  3180
         TTCAAACCTTCTTGGGGTGTAAAAAGGACGCGCAGTAGAGACTGTGCCGGAGGGAGACGA
```

```
a        K  F  G  R  T  P  H  F  S  C  A  S  S  L  T  R  P  P  S  A  -
b        S  L  E  E  P  H  I  F  P  A  R  H  L  *  H  G  L  P  L  L  -
c        V  W  K  N  P  T  F  F  L  R  V  I  S  D  T  A  S  L  C  Y
```

```
         ACTCCATCCTGAAAGCCAACAACGCACGGATGTCGCTGGGGGCCAAGGGCGCCGCCGCC
3181     ---------+---------+---------+---------+---------+---------  3240
         TGAGGTAGGACTTTCGGTTGTTGCGTGCCTACAGCGACCCCCGGTTCCCGCGGCGGCGG
```

```
a        T  P  S  *  K  P  R  T  Q  G  C  R  W  G  P  R  A  P  P  A  -
b        L  H  P  E  S  Q  E  R  R  D  V  A  G  G  Q  G  R  R  R  P  -
c        S  I  L  K  A  K  N  A  G  M  S  L  G  A  K  G  A  A  G  F  -
```

```
         CTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTC
3241     ---------+---------+---------+---------+---------+---------  3300
         GAGACGGGAGGCTCCGGCACGTCACCGACACGGTGGTTCGTAAGGACGAGTTCGACTGAG
```

```
a        L  C  P  P  P  P  C  S  G  C  A  T  K  H  S  C  S  S  *  L  -
b        S  A  L  R  G  R  A  V  A  V  P  P  S  I  P  A  Q  A  D  S  -
c        L  P  S  E  A  V  Q  W  L  C  H  Q  A  F  L  L  K  L  T  R  -
```

```
         GACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCTAGACGCAGCTGA
3301     ---------+---------+---------+---------+---------+---------  3360
         CTGTGGCACAGTGGATGCACGGTGAGGACCCCAGTGAGTCCTGTCGGCTCTGCGTCGACT
```

```
a        D  T  V  S  P  T  C  H  S  W  G  H  S  G  Q  P  R  R  S  *  -
b        T  P  C  H  L  R  A  T  P  G  V  T  Q  D  S  P  D  A  A  E  -
c        H  R  V  T  Y  V  P  L  L  G  S  L  R  T  A  Q  T  Q  L  S  -
```

FIGURE 51 (cont.)

```
         GTCCGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGCACTGC
3361     ---------+---------+---------+---------+---------+---------- 3420
         CAGGCTTCGAGGGCCCCTGCTGCGACTGACGGGACCTCCGCCCTCGGTGGGCCGTGACG
```

```
a        V  G  F  F  R  G  R  R  *  L  F  W  P  P  Q  F  T  R  H  C    -
b        E  E  A  F  G  D  D  A  D  C  P  G  G  R  E  Q  P  G  T  A    -
c        R  K  L  F  G  T  T  L  T  A  L  E  A  A  A  N  P  A  L  P    -
```

```
         CCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCTGCCCACAGCCAGGCCGAGAGCA
3421     ---------+---------+---------+---------+---------+--------- 3480
         GGAGTCTGAAGTTCTGGTAGGACCTGACTACCGGTGGACGGGTGTCGGTCCGGCTCTCGT
```

```
a        P  Q  T  S  F  F  S  W  T  D  G  H  F  F  T  A  R  P  R  A    -
b        L  R  L  Q  D  H  P  G  L  M  A  T  R  P  Q  F  G  R  E  Q    -
c        S  D  F  K  T  I  L  D  *  W  P  P  A  H  S  Q  A  E  L  R    -
```

```
         GACACCAGCAGCCCTCTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACAC
3481     ---------+---------+---------+---------+---------+--------- 3540
         CTGTGGTCGTCGGGACAGTGCGGCCCGAGATGCAGGGTCCCTCCCTCCCCGCCGGGTGTG
```

```
a        D  T  S  S  P  V  T  P  G  S  T  S  Q  G  G  R  G  G  P  H    -
b        T  P  A  A  L  S  R  R  A  L  R  P  R  E  G  G  A  A  H  T    -
c        H  Q  Q  P  C  H  A  G  L  Y  V  P  G  R  E  G  R  P  T  P    -
```

```
         CCAGGCCCGCACCGCTGGGAGTCTCACGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGT
3541     ---------+------ --+---------+---------+---------+--------- 3600
         GGTCCGGGCGTGGCGACCCTCAGAGTGCGGACTCACTCACAAACCGGCTCCGGACGTACA
```

```
a        P  G  P  H  R  W  E  S  E  A  *  V  S  V  W  P  R  P  A  C    -
b        Q  A  R  T  A  G  S  L  R  P  E  *  V  F  G  R  G  L  H  V    -
c        P  P  A  P  L  G  V  *  G  L  S  E  C  L  A  E  A  C  M  S    -
```

```
         CCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTCTCCACCCAAGGCCTGAGTC
3601     ---------+-     -----+---------+---------+---------+---------- 3660
         GGGCCGACTTCCGACTCACAGGCCGACTCCGGACTCGCTCAGAGGTCGGTTCCGGACTCAG
```

```
a        P  A  E  G  *  V  S  G  *  G  L  S  E  C  P  A  R  C  *  V    -
b        R  L  F  A  R  C  P  A  E  A  *  A  S  V  Q  P  R  A  E  C    -
c        G  *  P  L  S  V  R  L  R  P  E  R  V  S  S  Q  G  L  S  V    -
```

```
         TCCAGCCACACCTGCCGGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCACGGCC
3661     ---------+---------+---------+---------+---------+---------- 3720
         AGGTCGGTGTGGACGGCAGAAGTGAAGGGGTGTCCGACCGCGAGCCGAGGTGGGGTCCGG
```

```
a        S  S  F  P  A  V  F  T  S  P  Q  A  G  A  R  L  H  P  R  A    -
b        P  A  H  L  P  S  S  L  P  H  R  L  A  L  G  S  T  P  G  P    -
c        Q  H  T  C  R  L  H  F  P  T  G  W  R  S  A  P  P  Q  G  Q    -
```

```
         AGCTTTTCCTCACCAGCAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGA
3721     ---------+---------+---------+------ --+---   -         -+ 3780
         TCGAAAAGGAGTGGTCGTCGGGCCGAAGGTGAGGGGTGTATCCTTATCAGGTAGGGGTCT
```

```
a        S  F  S  S  P  G  A  R  L  P  L  P  T  *  E  *  S  T  P  P
b        A  P  P  H  Q  E  P  G  F  H  S  P  H  R  N  S  P  S  P  D    -
c        L  F  L  T  R  S  P  A  S  T  P  H  I  G  I  V  H  P  Q  T    -
```
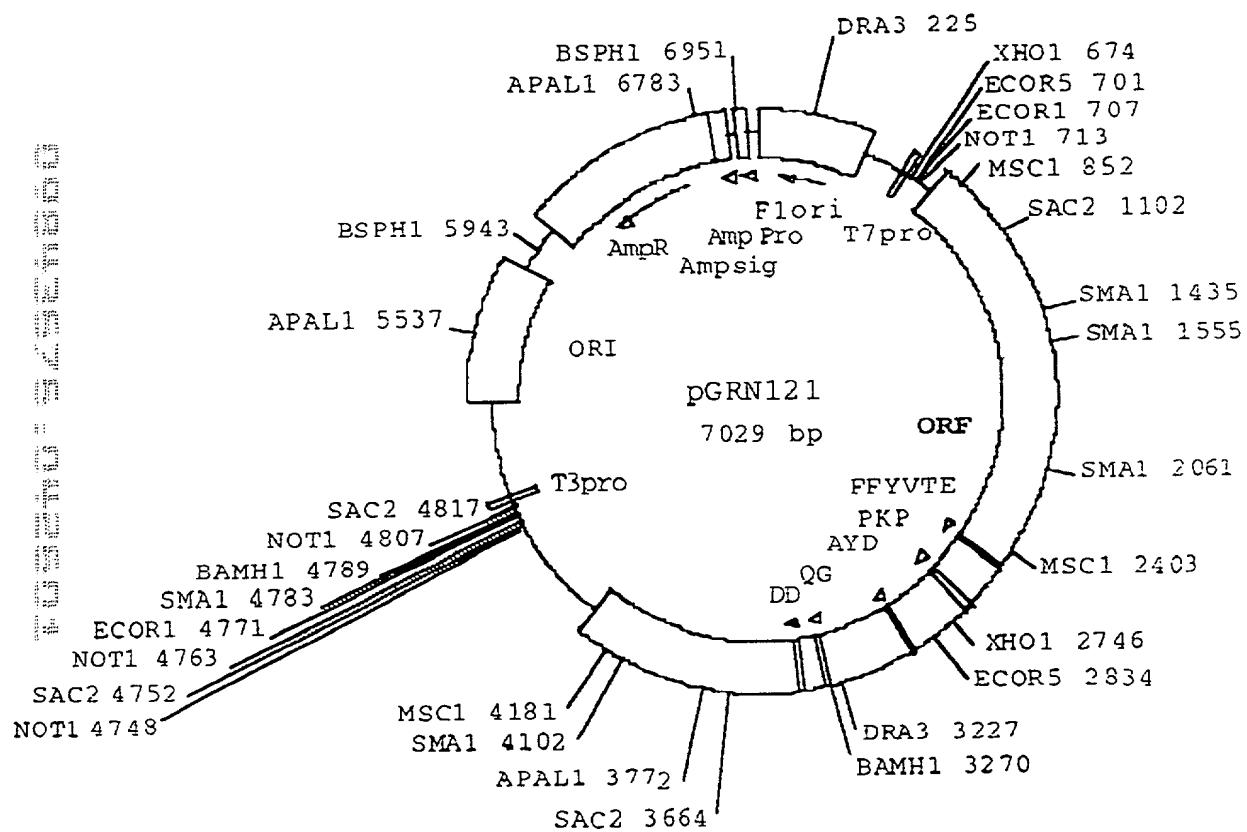
FIGURE 51 (cont.)

```
      TTCCCCATTGTTCACCCCTCGCCCTGCCCTGCTTTGCCTTCCACCCCCACCATCCAGGTC
5781  ----------+---------+-------- -+ --------+---------+---------, 3840
      AAGCGGTAACAAGTGGGGAGCGGGACGGGACCAAACGGAAGGTGGGGGTGGTAGGTCCAC


a     F  A  I  V  H  P  S  P  C  P  P  L  P  S  T  P  T  I  Q  V   -
b     S  F  L  F  T  P  P  A  L  L  C  L  P  P  P  P  S  R  W   -
c     R  H  C  S  P  L  A  L  P  S  P  A  F  H  P  H  H  F  G  G  -


      GAGACCCTGACAAGCACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTG
3841  ----------+---------+----------+---         +- --------+--------- 3900
      CTCTGGGACTGTTCCTGGGACCCTCGACACCCTTAAACCTCACTGGTTTCCACACGGGAC


a     E  T  L  R  A  L  G  A  L  G  I  W  S  D  Q  R  C  A  L   -
b     R  P  *  E  G  P  W  E  L  W  E  F  G  V  T  K  G  V  P  C  -
c     D  P  D  P  D  P  G  S  S  G  N  L  E  *  P  K  V  C  P  V-


      TACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGT
3901  ---------+---------+---------+---------+- -- - --+---------+ 3960
      ATGTGTCCGCTCCTGGGACGTGGACCTACCCCCAGGGACACCCAGTTTAACCCCCCTCCA


a     Y  T  G  E  D  P  A  P  G  W  G  S  L  W  V  K  L  G  G  C   -
b     T  Q  A  R  T  L  H  L  D  G  G  P  C  G  S  N  W  G  E  V  -
c     H  R  R  G  P  C  T  W  M  G  V  P  V  G  Q  I  G  G  R  C


      GCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAAAAAAAAAAAA
3961  ---------+---------+---------+---------+---------+---------, 4020
      CGACACCCTCATTTTATGACTTATATACTCAAAAAGTCAAAACTTTTTTTTTTTTTTTTT


a     A  V  G  V  K  Y  *  I  Y  E  F  F  S  F  E  K  K  K  K  K
b     L  W  E  *  N  T  E  Y  M  S  F  S  V  L  K  K  K  K  K  K
c     C  G  S  K  I  L  N  I  *  V  F  Q  F  *  K  K  K  K  K  K-


      AAAAAAAAA
4021  --------- 4029
      TTTTTTTTT


a     K  K  K   -
b     K  K   -
c     K  K   -
```

FIGURE 52

FIGURE 53

```
                                                                 1
                                                                met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG


                                   10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC


                    20                                        30
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG


                                   40
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT


                    50                                        60
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC


                                   70
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC


                    80                                        90
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC


                                   100
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG


                    110                                       120
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC


                                   130
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG
```

FIGURE 53 (cont.)

        140   150

```
          140                                          150
trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC


                              160
leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC


          170                                          180
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC


                              190
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT


          200                                          210
leu gly cys glu arg ala trp asn his ser val arg glu ala gly
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG


                              220
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC


          230                                          240
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC


                              250
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG


          260                                          270
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT


                              280
val val ser pro ala arg pro ala glu glu ala thr ser leu glu
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG
```

FIGURE 53 (cont.)

```
                290                                                  300
gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC


                                          310
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC


                320                                          330
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC


                                          340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA


                350                                          360
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG


                                          370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC


                380                                          390
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC


                                          400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG


                410                                          420
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA


                                          430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG
```

FIGURE 53 (cont.)

```
                440                                                              450
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG


                                               460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG


                470                                              480
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG


                                        490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC


                500                                              510
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG


                                        520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT


                530                                              540
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG


                                        550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG


                560                                              570
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC


                                        580
arg leu phe phe tyr arg pro ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG CCG AGT GTC TGG AGC AAG TTG CAA AGC


                590                                              600
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG
```

FIGURE 53 (cont.)

```
                                      610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG


        620                                           630
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG


                            640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC


            650                                   660
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG


                                      670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG


            680                                   690
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC


                            700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG


        710                                           720
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC


                            730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG


        740                                           750
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC


                            760
his gly his val arg lys ala phe lys ser his val ser thr leu
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG
```

FIGURE 53 (cont.)

```
          770                                              780
thr asp leu gln pro tyr met arg gln phe val ala his leu gln
ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG


                                  790
glu thr ser pro leu arg asp ala val val ile glu gln ser ser
GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC


          800                                              810
ser leu asn glu ala ser ser gly leu phe asp val phe leu arg
TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC


                                  820
phe met cys his his ala val arg ile arg gly lys ser tyr val
TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC


          830                                              840
gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu
CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC


                                  850
cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly
TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG


          860                                              870
ile arg arg asp gly leu leu leu arg leu val asp asp phe leu
ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG


                                  880
leu val thr pro his leu thr his ala lys thr phe leu arg thr
TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC


          890                                              900
leu val arg gly val pro glu tyr gly cys val val asn leu arg
CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG


                                  910
lys thr val val asn phe pro val glu asp glu ala leu gly gly
AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC


          920                                              930
thr ala phe val gln met pro ala his gly leu phe pro trp cys
ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC
```

FIGURE 53 (cont.)

```
                                        940
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

              950                                 960
ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

                              970
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

              980                                 990
val leu arg leu lys cys his ser leu phe leu asp leu gln val
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

                              1000
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

              1010                                1020
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

                              1030
his gln gln val trp lys asn pro thr phe phe leu arg val ile
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

              1040                                1050
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

                              1060
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

              1070                                1080
ser glu ala val gln trp leu cys his gln ala phe leu leu lys
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

                              1090
leu thr arg his arg val thr tyr val pro leu leu gly ser leu
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC
```

FIGURE 53 (cont.)

```
           1100                                                        1110
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG


                                  1120
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC


           1130      1132
phe lys thr ile leu asp OP
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCCACAGCCAGGCCGAGAGCAGA

CACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACACCC

AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC

GGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTC

CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG

CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT

CGCCATTGTTCACCCYTCGCCCTGCCYTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA

GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA

CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGCGGGGGAGGTGC

TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGRAAAAAAAAAAAAAAAAAA

AAAAAAAAAA
```

FIGURE 54

KPN1 17050
KPN1 18560
ECOR1 19475
SAC1 19652
SAC1 21083
ECOR1 23539
SAC1 24607
SAC1 29043

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